AR028488 Sequence I55851 Sequence 14 U19143 Human GAGE-AF055473 Homo sapi AR028491 Sequence

AF055473 AR028491

155854 Sequence 17
AX331451 Sequence 17
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AX284300 Sequence
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AX20842 Sequence
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AX208978 Sequence

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     GenCore version 4.5
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Sequence Homo sapi Sequence

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AX063165 Sequence
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AX204315 Sequence
AX204507 Sequence
AX2256542 Sequence
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Unclassified.
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van der Bruggen,P., van den Eynde,B., DeBacker,O. and
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Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens,
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PATORODPAAAQEGEDEGASAGGGPKPEAHSGEGGHPQTGCCECEDGPDGGEMDPPNPE
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Direct Submission
Submitted (28-DEC-1994) Benoit J Van Den Eynde, Ludwig Institute
For Cancer Research, 74 Avenue Hippocrate, BRUSSELS, 1200, BELGIUM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.
and Boon,T.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

De Backer, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C.,

Czekay, S., Viars, C.S., De Plaen, E., Brasseur, F., Chomez, P., Van de Eynde, B., Boon, T. and van der Bruggen, P.

Characterization of the GAGE genes that are expressed in various characterization of the GAGE genes that are expressed in various cancer Res. 59 (13), 3157-3165 (1999)
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De Backer, O.R.Y.
Direct Submission
Submitted (24-MAR-1998) Lupwig Institute for Cancer Research,
Brussels Branch, 74 av. HippOcrate, Brussels B-1200, Belgium
Location/Qualifiers
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100.0%; Pred. No. 5.7e-118;
.ive 0; Mismatches 0;
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Homo sapiens GAGE-8 mRNA, complete cds.
AF055473
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/db_xref="taxon:9606"
73. .423
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              Best_Local Similarity 100.
Matches 530; Conservative
             Similarity
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PAT 29-SEP-1999
/protein_id="AAC33676.1"
/db_xxef="61:1811023"
/translation="MWMRGRSTYRPRERRYVEPPEMIGPMRPEQFSDEVEPATPEEGE
PATQRQDPAAAQEGEDEGASAGQGPRPEADSQEQHPQTGCECEDGPDGQEMDPPNPE
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Pred. No. 7.3e-117;
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van der Bruggen,P., van den Eynde,B., De
Boon-Falleur,T.
Isolated peptides derived from the gage
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Patent: US 5858689-A 17 12-JAN-1999;
Location/Qualiflers
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AR028491
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98.3%;
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1 (bases 1 to 532)

Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.

Isolated peptides derived from tumor rejection antigens, and
                                        GCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
                                                                                                         AGCIGIGAGGCAGIGCIGIGGTICCIGCCGICCGGACTCTITITCCICTACTGAGAIT
                                                                                                                                                                CTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATA
                                                                                                                               TGGAACCAGCAACATCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
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 Score 504.8; DB 6;
Pred. No. 7.1e-112;
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Pred. No. 7.1e-112;
0; Mismatches 7;
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                0; Mismatches
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93.8%;
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Best Local Similarity 98.1%;
Matches 522; Conservative (
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1 (sites)
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 09-JAN-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                    CTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATA
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Pred. No. 4.7e-111;
0; Mismatches 6;
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/db_xref="taxon:9606"
114 c 156 g 11:
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Location/Qualifiers
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Consess 1 to 527)
Van Den Eynde, B.J.

Direct Submitssion
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
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                                                                                                                                                                                                                                                                        TGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAA 418
            1 | CGCCAGGGAGCTGTGAGGCAGTGCTGTGCTTCCTGCCGTCCGGACTCTTTTCCTCTA 60
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CGCCAGGGAGCTGTGAGGCAGTGCTGTGGTTCCTGCCGTCCGGACTCTTTTCCTCTA
                                                    CTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAG
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/protein_id="AAA82749.1"
/db_xref="GI:914909"
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/sex="female"
/cell_line="Mz2-MEL.43"
/tissue_type="melanoma"
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Mammalia; Eutheria;
1 (bases 1 to 527)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new family of genes coding for an antigen recognized autologous cytolytic T lymphocytes on a human melanoma J. Exp. Med. 182 (3), 689-698 (1995)
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/protein_id="AAA82747.1"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="female"
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/dev_stage="adult"
83. .436
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Chen, M.E., Lin, S.-H., Chung, L.W.R. and Sikes, R.A.
Isolation and characterization of PAGE-1 and GAGE-7: new genes
expressed in the LNCaP prostate cancer progression model that share
homology with melanoma associated antigens
J. Biol. Chem. (1998) In press
Chen, M.E., Lin, S.-H., Chung, L.W.R. and Sikes, R.A.
Direct Submission
Submitted (07.APR-1998) Urology, University of Virginia, Box 422,
Charlottesville, VA 22908, USA
                                                                                                          1;
/translation="MSWRGRSTYYWBRPRRYVQPPEVIGPMRPDGFSDBVEPATPEEG
EBTQRQDDBAAAQEGEDBGASAAQGPKPEADSQEQGHPQIGCECEDGPDGQEVDPPNP
EBTWRTPREGRKQQGV
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2e-110;
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Best Local Similarity 98.1%;
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/translation="mgwrgrstyywprprryvqppemigpmrpggfsdevepatpeeg
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                            /product="melanoma antigen related GAGE-7"
/protein_id="AAC25989.1"
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Pred. No. 3.9e-110;
2; Mismatches 6;
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/note="similar to GAGE family
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Human GAGE-5 protein m
U19146
U19146.1 GI:914906
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ilarity 97.9%;
Conservative
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Van den

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                       PRI 01-MAY-2000
                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 526)
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De Backer,O.R.Y.
Direct Submission
Submitted (34-MAR-1998) Ludwig Institute for Cancer Research,
Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
Locatlon/Qualifiers
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Similarity 98.4%; Pred. No. 8.2e-108;
14; Conservative 0; Mismatches 5;
            AF055474 526 bp mRNA Homo sapiens GAGE-7B mRNA, complete cds. AF055474
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/db_xref="taxon:9606"
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504;
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DEFINITION
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/product="GAGE-5 protein"
/product="GAGE-5 protein"
/protein_id="AAA82748.1"
/db_xref="G1::014907"
/translation="MSWRGRSTYYWPRPRRYVQPPEVIGPMRPEQFSDEVEPATPEEG
FATORQDPAAAQEGEDEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGGEMDPPNP
                                                                                                                    Cases 1 to 524)
Van Den Eynde, B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
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                                             bγ
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        Gaugler, B.,
                 A new family of genes coding for an antigen recognized autologous cytolytic T lymphocytes on a human melanoma J. Exp. Med. 182 (3), 689-698 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 496.8; DB 9; Length 524;
Pred. No. 6.1e-110;
0; Mismatches 7; Indels 3
Van den Eynde, B., Peeters, O., De Backer, O., and Boon, T.
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                                                                                                                                                                                                                                               1. .524
/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                                                                                                                                                                                           /cell_line="MZ2-MEL.43"
                                                                                                                                                                                                                                                                                                                                            /tissue_type="melanoma"
/dev_stage="adult"
75. .428
                                                                                                                                                                                                                         Location/Qualifiers
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Best Local Similarity 98.1%;
Matches 514; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (14-AUG-2001) Zendman A.J.W., Department of Pathology,
University Medical Center St Radboud, Geert Grooteplein Zuid 24,
Box 9101 6500 HB Nijmegen, NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression profile of members of the XAGE cancer/testis antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (sites)
Lillie,J., Brown,J.L., Bolt,A. and van Huffel,C.
Novel genes, compositions and methods for the identification, assessment, prevention, and therapy of human cancers Patent: WO 0179556-A 497 25-OCT-2001;
Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGAACGTTGAAATGATGCA
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Muijen,G.N.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.6%; Score 299.2; DB 6; Length 365; 95.9%; Pred. No. 4e-62; ive 0; Mismatches 13; Indels 0
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                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
1 86 c 66 q 150
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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XAGE-3 gene.
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Zendman, A.J.W.
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Matches 307; Conservative
                                       Homo sapiens
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
235 ATCCTGCAGCTGCTCAGGAGGGAGGGATGAGGGATCTGCAGGTCAAGGGCCGAAGC 294 [1111] [1111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11
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Sequence 105 from Patent WO0179556.
AX284300
                                                                                           507 CTTTACAGCCTTCTGCAAAGAAAAAAAA 538
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100 c 106 q 183
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33.9%; Score 182.4; DB 9; Length 493;
Best Local Similarity 68.9%; Pred. No. 7.3e-34;
Matches 317; Conservative 0; Mismatches 121; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 ITCICCCAAIAAAGCITIACAGCCTICIGCAAAGAAAAA 532
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61. 396
61. 396
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_hum:\*
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em\_gss\_pln:\*
em\_gss\_vrt:\*

em\_estba:\*
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Database :

		Description			а.	AA447559 zw81e11.s	_		AA738037 nx15e11.s	AW016546 UI-H-BI0p			_	AI187350 qf29a05.x	AW102587 xd67g07.x	BC005363 Homo sapi	AA448542 zw81e11.r	AA913206 om53f03.s	BG206349 RST25797	AA918604 o153f02.s	
SUMMARIES		10 th	- !	527 10 BI826605	509 10 BI868671	489 9 AA447559	457 9 AW510753	447 9 AI381509	6	418 9 AW016546	10	426 9 AA868226	6	455 9 AI187350	412 9 AW102587	445 11 BC005363	419 9 AA448542	0	10	398 9 AA918604	•
	æ	Query	שמרכון הבו	91.4	98.6	84.1	80.2	78.9	78.9	16.97	76.8	76.7	76.4	74.6	67.9	67.0	8.99	61.3	5.65	55.1	
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## ALIGNMENTS

B1826605 527 bp mRNA linear EST 04-OCT-2001 603077056F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5168892 5', mRNA sequence. B1826605 . B1826605.1 GI:15938155 EST. Human.	Eukaryota; Metazoa; Chordata; Craniaca; Verebiaca; Eucazoacomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 527)  NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  Contact: Robert Strawberg, Ph.D.	Tissue procurement: Life Technologies, Inc.  CDNA Library Preparation: Life Technologies, Inc.  CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Incyte Genomics, Inc.  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  http://mage.llnl.gov. p column: 13  High quality sequence stop: 519.	1527  /organism="Homo sapiens" /organism="Homo sapiens" /db_xref="Laxon:9606" /clone=lib="NIH_MGC_119" /fissue_rype="medulia" /fissue_rype="medulia" /lab_host="DH108" /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source normal medulia from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range
RESULT 1 B1826605 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT		FEATURES SOURCE

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:5402663"
/clone=lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/tab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Sall; cloned unidirectionally; oligo-dr primed.
Site_2: Sall; cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ACTGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGAC---TATCGGCCTA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 GACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCA
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al Similarity 98.0%; Pred. No. 1.3e-100;
494; Conservative 0; Mismatches 7;
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Location/Qualifiers
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BI868671
BI868671.1 GI:16042344
EST
0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                        Score 492; DB 10;
Pred. No. 3.8e-104;
0; Mismatches 5;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                        91.48;
98.38;
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Gaps 9 65 185

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1 (bases 1 to 48)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lary, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle
, T., Waterston, R. and Wilson, R.
WashU warck EST Project 1997
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Park Washington University School of St. Louis, MO 63108
Tel: 314 286 1800
Fex: 314 286 1810
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                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -4nml3 fwd. Er from Amersham High quality sequence stop: 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 GTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCACAGACTGGGTGT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 AGTGTGAAGATGGTCCTGATGGGCAGGAGTGGACCGCCAAATCCAGAGGAGGAGGTGAAAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 CCGGACTCTTTTCCTCTACTGAGATTCATCTGTGAAATATGAGTTGGCGAGGAAGAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 CGACC---TATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 CAACTCAACGTCAGGATCCTGCAGCTGCTCCAGGAGGAGGAGGAGGAGGAGGAGCATCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 CAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 CGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAAGAAGACACGTTGAAATGATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 GCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCCAATAAAGCTTTACAGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 GTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACACACTGGGTGTG
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

84.1%; Score 452.4; DB 9; Length 489;
Best Local Similarity 98.0%; Pred. No. 6e-95;
Matches 480; Conservative 0; Mismatches 6; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:782636"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                   1. .489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
        REFERENCE AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                       COMMENT
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1. 457

/organism="Homo sapiens"
/db_zere[="Laxon:9606"
/clone="ImAGE:2911881"
/clone="InbaGE:2911881"
/clone="InbaGE:2911881"
/clone="InbaGE:2911881"
/rote="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-Cell NCI_CGAP_GCB1) were mixed, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
87 a 133 c 95 g 142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                               AW510753 457 bp mRNA linear EST 03-MAR-2000 hd39d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2911881 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 457)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -dOUP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 GTGAAATATGAGTTGGCGAGGAAGATCGACCTATC---GGCCTAGACCAAGACGCTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 GGGGGGGGGGGGGGGGGCAGCATCTGCGAGGGCCGAAGCCTGAAGCTCATAGCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.2%; Score 431.4; DB 9;
1larity 98.0%; Pred. No. 4.5e-90;
Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                             mRNA sequence.
AW510753
AW510753.1 GI:7148831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                 10 TGCAAAGAAA 1
                                                            520 TGCAAAGAAA
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNT
                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                              RESULT 4
AW510753/c
                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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/note—"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI, Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAA_GCB1) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                AI381509 447 bp mRNA linear EST 28-MAR-1999 te76b07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN. ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 497 Std Error: 0.00
Seq primer: -40UP from Gibco.
                                                                                          433
                                                                                                                                                                     AAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTTGTTCATTAAAAT 493
                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 GTTGGCGAAGAACTCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACACCCTCG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGGCGAGGAAGATCGACC --- TATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                        ACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGA
                                                                                 CCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTA
                                                                                                                                                                                                           97 AAAGAAGGCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAAT
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/db_xref="taxon:9606"
/clone="IMAGE:2092597"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Pred. No. 1.7e-88;
0; Mismatches 4
                                                                                                                                                                                                                                                     TCTCCCAATAAAGCTTTACAGCCTTCTGCAAAAA 530
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                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI381509
AI381509.1 GI:4194290
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Best Local Similarity 98.4%;
Matches 440; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
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                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                          RESULT 5
AI381509/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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COMMENT
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ORIGIN
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MINION 11:01 NCI_CGAP_CC3 Homo sapiens CDNA clone IMAGE:1256204 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN.; mRNA sequence. AA738037.1 GI:2768794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 464)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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                                                                              264
                                                                                                                     268
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                    AAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACTG
                                                                                                                                                                                                                                   325 CACAGACTGGGTGTGAGGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATC
                                                                                                                                                                                                                                                                                                               385 CAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACAC
                                                                                                                                                                                                                                                                                                                                    445 GITGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAA
                                                                                                                                                        265 AGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACC
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 511 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 435.
Location/Qualifiers
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/Gogalism="Homo sapiens"

/GD_xref="taxon:9606"

/clone="IMAGE:1256204"

/clone=lib="NoT_CGAP_GG3"

/tissue_type="pooled germ cell tumors"

/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTTTACAGCCTTCTGCAAAGAAAA 531
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                              ATGAGTTGGCGAGGAAGATCGACC ---TATCGGCCTAGACCAAGACGTACGTAGAGCCT 140
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vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. 132 c -93\ g 153 t
                                                                                                                                                                                                                                                            104 GCACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCA
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                                                                                                                                                                                                                                                                                                                                     Length 464;
                                                                                                                   11; Indels
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Pred. No. 1.9e-88;
0; Mismatches 11.
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1. .418
                                                                                      78.9%;
96.9%;
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                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                242 AGCTGCTCAGGAGGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGC
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                                                                                                                                                                                             Length 418;
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                                                                                                                                                                                             76.9%; Score 413.8; DB 9 99.5%; Pred. No. 5.5e-86; tive 0; Mismatches 2
                                                                                                                                                                                                        Matches 415; Conservative
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468 TAIGITGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 76.7%;
al Similarity 97.9%;
417; Conservative
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                                                                                                                                                       435 AAAAAAAAAA 445
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                                                                                              BG120336 480 bp mRNA linear EST 30-JAN-2001
602353732F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451958 5',
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 480) NHT-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="adenocarcinoma, cell line"
/tab_host="bH10B (phage-resistant)"
/note="longan: liver; Vector: pCWN-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.7 kb. Library enriched for
full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Lncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
http://image.llnl.gov
Plate: Libral0239 row: p column: 07
High quality sequence stop: 480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 GAGCAGTICAGIGAIGAAGIGGAACCAGCAACACCIGAAGAAGGGGAACCAGCAACICAA 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 GATGGTCCTGATGGCCAGAGATGGACCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 CGTCAGGATCCTGCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGG
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11arity 97.4%; Pred. No. 6.8e-86;
Conservative 0; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .480
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone-"IMAGE:4451958"
/clone_lib="NIH_MGC_90"
                                                                                                                                                                BG120336.1 GI:12613845
                                                                                                                                 mRNA sequence.
BG120336
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EST 16-MAR-1998
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information can be
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AA868226 426 bp mRNA linear EST 16-MAR-1998
ak48h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409245
3' similar to SW:GGE2_HUMAN Q13066 GAGE-2 PROTEIN. [1] ;, mRNA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
                                                                                                                                                                                                                                 1 (bases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contect: Robert Strausberg, Ph.D.
Contect: Gobert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 TCGACCTATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution: found through the I.M.A.G.E. Consortium/Lini at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 412.8; DB 9;
Pred. No. 9.4e-86;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1409245"
/clone_lib="Soares_testis_NHT"
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
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12 I (Dases 1 to 450)

13 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

14 Tumor Gene Index

15 Tumor Gene Index

16 Tumor Gene Index

17 Tumor Gene Index

18 Tumor Gene Index

18 Tumor Gene Index

19 Tumor Gene Index

10 Tumor Gene Index

10 Tumor Gene Index

11 Saue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Enmil: ogapbs remail.infl.gov

17 Issue Procurement: Christopher A. Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.

18 Tumor Library Preparation: M. Bento Soares, Ph.D.

19 CDNA Library Preparation: M. Bento Soares, Ph.D.

10 CDNA Library Arrayed by: Greg Lennon, Ph.D.

10 Na Sequencing by: Washington University Genome Sequencing Center

11 Tumory Cybry Jimage/Aimage.html

11 Seq primer: -40ml3 fwd. ET from Amersham

11 High quality sequence stop: 331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nx32h08.s1 NCI_CGAP_GC4 Homo sapiens cDNA linear EST 26-JAN-1998 similar to TR:Q13070 Q13070 GAGE-6 PROTEIN.;, mRNA sequence. AA760996 AA760996.1 GI:2809926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /.uc.tell.whGE:127855"
/clone="iMAGE:127855"
/clone=lib="NCI_CGAP_GC4"
//tssue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 450)
                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                         402 CCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGC 461
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                                                                                                                                                                                                                                                                                                                                                                                      246 CAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCACAGAGACTGGTGAG
                  186 TGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCCCCAAATCCAGAGGAGGAGGAGAAACG
                                                                                                                                                                                                                                                                                                                              126 CCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGGAGGTGTGAAATGATGCAGGC
*CGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGGAACCAGCA
                                                                          222 ACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGGAGCATCTGCAGGT
                                                                                                                                                    CAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAG
                                                                                                                                                                                                                                 TGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACG
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/db_xref="taxon:9606"
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cona Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 504 Std Error: 0.00
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI187350 455 bp mRNA linear EST 10-NOV-1998 qf29a05.xl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751408 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. [1] ;, mRNA
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Eukaryota...
Eukaryota...
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo...
I (bases I to 455)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap...
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
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                                                                                                                                                        84 ATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGACGCTACGTAGAGCCT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAAGAAG
                                                                                                                                                                           450 ATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGACCAAGGCGCTATGTACAGCCT
                                                                                                                         4
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Bonaldo.
                                                                                Score 410.8; DB 9;
Pred. No. 2.7e-85;
0; Mismatches 8;
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Fatima
140 t
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Location/Qualiflers
Σ. Q.
and
94
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A1187350
A1187350.1 GI:3737988
 Bento Soares
130 c
                                                                                        Query Match 76.4%;
Best Local Similarity 97.3%;
Matches 439; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
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/u.shall homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="inb="Soares"NFL_T_GBC_S1"
/lab_host="DH10B"
/rothe="organ:pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbH119W, testis NHT; and B-cell NCI_CGAP_GCB1) were mixed, and scircles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatlama Bonaldo.

78 a 114 c 84 g 133 t 3 others
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                                                       Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 285.
Location/Qualifiers
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 CCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGAGGGAACCA-GC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 CGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 AACACCTGAAGAAGGGGAACCAG-CAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 GAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 GAGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 AGGGTCACCCACACACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 AGGTCACCCACAGAGTGTGAGTGTGAGTGTGAGATGGTCCTGATGGCAGAGATGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 CGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAAGAGTGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.9%; Score 365.4; DB 9; 97.8%; Pred. No. 9.6e-75; ive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 TCCCAATAAAGCTTTACAGCCTTCTGCAAAGAAAAAAA 535
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Homo sapiens, clone IMAGE:3686872, mRNA.
BC005363.
BC005363.1 GI:14710126
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Unpublished (1997)
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                                                                                                                                 xd67g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2602716 3' similar to SW:GGE2_HUMAN Q13066 GAGE-2 PROTEIN. [1] i, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ATGAGTTGGCGAGGAAGATCGACCTAT - CGGCCTAGACCAAGACGCTACGTAGAGCCTC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 CTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACAC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 ATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 ACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCCGCCAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 ACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGACCGCCAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 ATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442 CACGITGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                Score 401.2; DB 9;
Pred. No. 4.6e-83;
0; Mismatches 18;
                                                                            /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 TAAAGCTTTACAGCCTTCTGCAAAGAAAAAAAA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 TAAAGCTTTCCAGCCTTCTGCAAAAAAAAA 1
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                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 95.4%;
Matches 435; Conservative 0
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                                                                                             /sex="male"
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GI:2162212
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                                                                             zw8lell.rl
5' similar
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Matches 390;
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CA 94305
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/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="IMAGE:3886672"
/tissue_type="Bone marrow, chronic myelogenous leukemia"
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                                                                                                                                                                                                                      CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@pax11.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                Euteleostomi;
                                                                           Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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               Craniata; Vertebrata; E
Catarrhini; Hominidae;
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                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Enall: cgapbs.r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 360.4; DB 11;
Pred. No. 1.4e-73;
0; Mismatches 16;
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102 c 132 g 8
               Chordata;
Primates;
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95.3%;
               Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 445)
Strausberg,R.
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 sapiens
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/clone__in___/sex="male"
/sex="male"
/lab_inost="DH10B"
/lab_inost="DH
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 419)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
419 bp mRNA linear EST 04-JUN-1997 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782636 to TR:G914905 G914905 GAGE-4 PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: estewatson wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@limage.llnl.gov) for further information.
Seq primer: -Zamil3 rev2 ET from Amersham
High quality sequence stop: 353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GACCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCAGAGCAGTTCA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
H444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:9606"
/clone="IMAGE:782636"
/clone_lib="Soares_testis_NHT"
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Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 487 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone="InAGE:155099"
/clone="InAGE:155099"
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/flab_nost="puploge"
/note="vector: pTyT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTyT3 vector. Library is normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo."

119 c 83 g 119 t
                                                                                                                                                                                                                                                                                                     AA913206 384 bp mRNA linear EST 17-JUN-1998 om53f03.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1550909 3' similar to SW:GGE3_HUMAN Q13067 GAGE-3 PROTEIN. [1] ;, mRNA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National cancer Institute, Cancer Genome Anatomy Project (CGAP),
                   238 CIGCAGCIGCICAGGAGGAGGAGGAIGAGGGAGCAICIGCAGGICAAGGGCCGAAGCCIG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 GATCGACCTATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTA 159
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                                                                                                                                                            AA913206.1 GI:3052598
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Matches 343; Conservative
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AA913206/c
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ORGANISM
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VERSION
KEYWORDS
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AUTHORS
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Search completed: July 1, 2002, 07:07:18 Job time: 1784 sec

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July 1, 2002, 06:39:24; Search time 177.44 Seconds (without alignments) 5205.703 Million cell updates/sec
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538
1 ACGCCAGGGAGCTGTGAGGC.......CTGCAAAGAAAAAAAA 538
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                        - nucleic search, using sw model
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Maximum DB seq length: 538
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	GAGE-2 tumour reje	GAGE-5 tumour reje	cDNA encoding GAGE	CDNA encoding GAGE	Human secreted pro	Human cancer agent	Human cancer agent	Human polynucleoti	DNA encoding novel
SUMMARIES	DI	AAX90519	AAX90522	AAV18720	AAV18717	AAC02129	AAS60104	AAS60496	AA160530	AAS69484
	DB	20	20	19	19	21	22	22	22	23
	Query Match Length DB	538	532	532	535	430	530	365	532	503
dР	Query Match	100.0	93.8	92.3	91.6	66.5	56.0	55.6	36.1	32.0
	Score	538	504.8	496.8	493	357.8	301.4	299.2	194	172.4
	Result No.		7	ľ	4	2	ω U	7	8	6

Human NOV2 DNA. H Human Lung tumour Human prostate CDN Human prostate-spe Human prostate-spe Prostate tumour an Human ovarian PCR- Human ovarian tumo	roll8 EST 4 coding 1 ung tuffi 1 ung tuffi 1 munoge 1 -8335042 1 -8335042 1 ung tuffi NOVI DNA secreted lung tuffi lung tuffi con a clo	secreted private secret
AAD14981 AAF68151 AAS633900 AAH93807 AAH85121 AAH02872 AAS24637 AAS24637	AA295012 AA295013 AA295013 AAE68851 AAD6691 AAD14997 AAD14990 AAV41280 AAV41280 AAX41280 AAX45997	AAX55997 AAA12613 AAA12613 AAH129806 AAL133515 AAL132796 AAL27748 AAL37747 AAL37747 AAC3275 AAC6618 AAC6618 AAC6618
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Van Der Bruggen Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathólogical condition; cancer; CTL; cytolytic T lymphocyte; GAGE; ss. GAGE-2 tumour rejection antigen clone nucleotide sequence. Boon-Falleur T, Debacker O, Van Den Eynde B, AAX90519 standard; cDNA; 538 BP (LUDW-) LUDWIG INST CANCER RES 99WO-US00775. 98US-0012818. (first entry) W09937665-A1. Homo sapiens 23-JAN-1998; 12-JAN-1999; 29-JUL-1999. 30-SEP-1999 AAX90519; RESULT AAX90519 

New isolated peptides which bind to HLA-A29 molecules, which are tumour rejection antigens used for detection and therapy of WPI; 1999-469111/39.

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The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLS) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLS in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGAC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AGCTGTGAGGCAGTGCTGTGTGTGTTGCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATT
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                                                                                                                                                                                                  New isolated peptides which bind to HLA-A29 molectumour rejection antigens used for detection and pathological conditions, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 504.8; DB 20; 98.1%; Pred. No. 1.3e-136; ive 0; Mismatches 7;
                                                                                                                                             Van Den Eynde
                                                                                                                                                                                                                                                               Example 13; Fig 4; 62pp; English.
                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                             Boon-Falleur T, Debacker O,
                                                                                     98US-0012818.
                                                        99WO-US00775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.1
Matches 522; Conservative
                                                                                                                                                                         WPI; 1999-469111/39.
A09937665-A1
                                                        12-JAN-1999;
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                            29-JUL-1999
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                                                     The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic I lymphocytes (CTLS) in pathological conditions such as cancer and in HLA-Typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                   Length 538,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGE-5 tumour rejection antigen clone nucleotide sequence.
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                         Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 other;
                                                                                                                                                                                                                                Score 538; DB 20;
Pred. No. 3e-146;
0; Mismatches 0;
   e.g. cancer
                             English.
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cytolytic T lymphocyte; GAGE; ss
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Best Local Similarity 100.0%;
Matches 538; Conservative 0;
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conditions,
                            Example 13; Fig 4; 62pp;
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pathological
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Gaps 69 9

3;

Indels

DB 20; Length 532;

180

246 240 306

300 366 360

426

480

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The present sequence encodes a GAGE-5 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally ifferent from the other GAGE CDNAS for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Confirm a diagnosis of melanoma using cytolytic T cell clone confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-CW6 molecules into peptides, useful to diagnose melanomas
                                                                                                                                                                  tumour tumour rejection antigen precursor; TRAP; tumour; nosis; melanoma; antigen; cytolytic T cell clone proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 97.2%; Score 496.8; DB 19; Length 532; Similarity 97.2%; Pred. No. 2.7e-134; Pred. 0; Mismatches 12; Indels 3;
                                                                                                                                 cDNA encoding GAGE-5 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                                    aa:Ala)
aa:Thr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 other;
                                                                                                                                                                                                                                                                                                                 /transl_except= (pos:189..191, /transl_except= (pos:192..194,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Den Eynde
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Fig 4; 60pp; English.
                                  AAV18720 standard; cDNA; 532 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boon-Falleur T, Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US10850.
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                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                     .429
                                                                                                                                                                                   diagnosis; melanoma;
HLA-typing assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-076905/07.
P-PSDB; AAW47602.
                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1996;
                                                                                               30-JUL-1998
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Best Local Si
Matches 517;
                                                                  AAV18720;
                                                                                                                                                                  GAGE
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RESULT
AAV18720
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                                                                                                                                                                                                                                                        AGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA 486
                                                                                                               306
                                                                                                                                                            GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG 366
                                                                                                                                                                                                                                                                              421 agtgttaaaaagaaaggcacgttgaaatgatgcaggctgctcctatgttggaaatttgttca 480
catctgtgtgtgaaatatgagttggcgaggaagatcgacctattattggcctagaccaaggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation; HLA-typing assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding GAGE tumour rejection antigen
by HLA-Cw6 molecules into peptides, useful to
                    GCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
                                                                             gccaggaacagggtcacccacagactgggtgtgagtgtgaagatggtcctgatgggcagg
                                            ggtatgtacagcctcctgaagtgattgggcctatgcggcccgagcagttcagtgatgaag
                                                                                                               CTCAGGAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATA
                                                                  TGGAACCAGCAACATCTGAAGAAGAAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
                                                                                                                                                                                                                                                                                                    cDNA encoding GAGE-2 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aa:Ala)
aa:Thr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boon-Falleur T, Debacker O, Van Den Eynde B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                    AAV18717 standard; cDNA; 535 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid
precursor - processed
diagnose melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-076905/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                    127
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                            precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequences. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAs for the first 112 bases. This region of GAGE-3 whose 5' end is totally arbitrary and be used to disquose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 tactgagattcatctgtgtgaaatatgagttggcgaggaagatcgacctatcggcctaga 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356
                   sequence encodes a GAGE-2 tumour tumour rejection antigen
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
                                                                                                                                                                                                                                                      proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACGCCAGGGAGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTC-
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                                                                                                                                                                                                                                                                                                                                                       Length 535;
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                         Sequence 535 BP; 158 A; 112 C; 156 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                         91.6%; Score 493; DB 19; 97.2%; Pred. No. 3.5e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; cDNA; 430
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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es 524; Conserv
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited from isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact 5' ends and can therefore be used to obtain full length energy and genomic DNAs. 5' ESTs are also used in diagnostic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293
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                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ACTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTAT--CGGCCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 430 BP; 101 A; 102 C; 134 G; 85 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 357.8; DB 21;
Pred. No. 5.9e-94;
                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                       Giordano
                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 2127; 71pp + CD-ROM; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                       Duclert A,
chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.5%;
ilarity 97.6%;
Conservative
                                                                                                                                   21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                   99US-0122487
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                                                                                                                                                                                                                                     Dumas Milne Edwards
                                                                                                                                                                                                                                                                     2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 368; Conserv
                                                                                                                                                                                                                                                                                       P-PSDB; AAG02123
                                                                                                                                                                                                       (GEST ) GENSET
gene therapy;
                                 Homo sapiens
                                                                 EP1033401-A2
                                                                                                 06-SEP-2000
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TGGGCAGGAGATGGACC 375

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

354 359

q ά S

414 tgggcaggagatggamc 430

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The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers or the methods can be used to determine the effectiveness of TAXOL.

In the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, the markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of the targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), the present sequence is one of the 1046 novel cancer cell markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid, used as a marker to determine the effectiveness of using TAXOL to treat cancer cell growth in individuals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTGATGAAGTGGAACCAGG--AACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                              Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 530 BP; 89 A; 100 C; 106 G; 183 T; 52 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Huffel C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                              Human cancer agent-sensitive marker #105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 120; 527pp; English.
                                            BP
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                                 AASS0104 standard; cDNA; 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-2001; 2001WO-US12132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-APR-2000; 2000US-197538P
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-602933/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200179556-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                   29-JAN-2002
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Best Local Si
Matches 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L1111e J,
                                                                                                            AAS60104;
AAS60104/c
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ATCCTGCAGCTGCTCAGGAGGAGGAGGATGAGGACCATCTGCAGGTCAAGGGCCGAAGC 294

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markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The marker's can be used as targets in developing anti-cancer agents such as chemotherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcribts or genomic sequences corresponding to the markers, in the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pr cell marker; TAXOL; cytostatic; tumour; carcinoma;
l carcinoma; sarcoma; fibrosarcoma; leukaemia;
leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid, used as a marker to determine the effectiveness of using TAXOL to treat cancer cell growth in individuals -
                                                     1329 CTGAAGNTGATAGCCAGGAACAGGGTCNCCCCCANACTGGGNGTNAGTGTNAAAATGGTC 270
                                                                                                           414
389 ATCCTGNAGCTGCNCAGNAGGGANAGGATNAGGGNGCATNTGCAGGTCAAGGGCCGAAGC 330
                                                                                                                                                                                 474
                                                                                                                                                                                                                                                          475 GAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGAAAAAAA 534
                                                                                                                                                                                                                                                                                            90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to 1046 novel nucleic acids which are used as
                                                                                                                               CTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAAACGCCTGAAGAAGGTG
                                                                                                                                                                                    AAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTG
                                    CTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van Huffel C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cancer agent-sensitive marker #227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 231; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS60496 standard; cDNA; 365 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-APR-2001; 2001WO-US12132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-602933/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cancer cell
squamous cell carci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200179556-A2
                                                                                                                                                                                                                                                                                                                                   535 AAAA 538
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                                                                                                                                                                                                                                                                                                                                                                       89 AAAA 86
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           be targeted include carcinoma (e.g. squamous cell carcinoma), sarcoma (e.g. tibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046
                                                                                                                                                                                                                                                                                                                                       219 GCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCA 278
                                                                                                                                                                                        GAGTGTGAAAATGGTCCTGATGGGCAGGAAATGGACCCGCCAAATCCAAAGGAGGTGAAA 186
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                         GGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGGTGT
                                                                                                                                                                                                                                      GAGTGTGAAGATGGTCCTGATGGGCAGGAGGATGGACCCGCCAAAATCCAGAGGAGGTGAAA
                                                                                                                                                                                                                                                                                                                          ACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCA
                                                                                                                                                                                                                                                                                                                                                                           GCCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTT
                                                                                                                                                                                                                                                                                                                                                                                         protein. Cancers which may
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0
                                                                                                                            Length 365;
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es 13; Indels
                                                                                                                           22;
                                                                                      63 A; 86 C; 66 G; 150 T; 0 other
                                                                                                                            DB
                                                                                                                           Score 299.2; Dered. No. 5.7e-0; Mismatches
cells or tissues which mis-express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO 4519.
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                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAAAGAAAAAAAA 538
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
                                                                                                                         55.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AA160530 standard; cDNA; 532
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                                                              novel cancer cell markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                    Conservative
                                                                                                                         Query Match
Best Local Similarity
Matches 307; Conserv
                                                                                      Sequence 365 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 TACTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATCGGCCTAGA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
                                        Wang
                                                                                                                                                                    useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACGCCAGGGAGCTGTGAGGCAGTG-CTGTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 atgccctggagttgtgagggtgtgagggtcgcgttcctgctgctgtctggacttttctgtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGAAGTGGAACCAGCAACACCTGAAGAGGGGAACCAGCAACTCAACGTCAGGATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 gatgaggag------cctcagcaagaggaaccaccaactgaaagtcgggatcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGCTGCTCAGGAG - - - GGAGAGGATGAGGGGAGCATCTGCAGGTCAAGGGCCGAAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 gcacctggtcaggagaagaagaagatcagggtgcagctgagactcaagtgcctgacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 gaagetgateteceaggagetgtetecagteaaagaetggggatgaatgeggagatggteet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA-GAAGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 gatgtccaggggaagattctgacaaagtcagagcaatttaaaaatgccagaagggaggtga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGCAATCACAGTGTTAAAAGGAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caggcaaccacaggtttaaatgaagacaagctgaaacaacacaaaactgt.ttttatcta
                                      Ren F, W
Zhang J;
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                                      Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 532 BP; 154 A; 108 C; 150 G; 120 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.1%; Score 194; DB 22;
68.4%; Pred. No. 2.4e-46;
                                  tu C, Xue AJ,
Cu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                      ID NO 4519; 10078pp; English.
                                                                                                                                                                                     such as central nervous system injuries
                                                                                                                                                                    Novel nucleic acids and polypeptides,
                                    Asundi V, Chen R,
Wehrman T, Xu C,
Goodrich R, Drman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                              2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                    Liu C,
Wang Z,
                                                                         2hou P,
(HYSE-) HYSEQ INC
                                                                                                                               P-PSDB; AAM41374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification
                                                                                                                                                                                                                          Claim 1; SEQ
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Matches 365;
                                                        J,
QA,
                                      Tang YT,
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                                                                         Zhao
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The controlled sare also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and cannon acid sequences. AAS64197-AAS94564 represent novel human character coding sequences of the livention.

Note: The sequence data for this patent did not appear in the printed consistent but was otherwise forms dispersive the printed consistent but was otherwise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                 a mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 503 BP; 158 A; 98 C; 121 G; 105 T; 21 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
                                                                                                                                                                            DNA encoding novel human diagnostic protein #5288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 5288; 103pp; English.
                                         AAS69484 standard; cDNA; 503 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.0%;
Best Local Similarity 68.2%;
Matches 307; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-639362/73.
P-PSDB; ABG05297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                        Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                             food supplement;
                                                                                                                                                                                                                                                                                                                                 WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                13-FEB-2002
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                                                                                        AAS69484;
φ
                       AAS69484
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G-protein coupled receptor; GPCR, hepatocyte nuclear factor; mast cell protease; gene therapy; prollferative disorder; cancer; immune disorder; hepatic disorder; cirrhosis; viral infection; hepatitis; neurollactory system-related disorder; neurological disorder; parkinson's disease; infertility; autolimmune disease; arthritis; multiple sclerosis; allergy; wound healing; cytostatic; nootropic; immunosuppressive; neuroprotective; vulnerary; hepatotropic; ds.
136 AGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAG 195
                                                                                                      312
                                                                                                                              273
                                                                                                                                                         372
                                                                                                                                                                       432
                                                                                                                                                                                                                                  334 ttctgccaaaatcagaacaatttaaaatgccagaaggaggtgacaggcaaccacaggttt 393
                                                                                                                                                                                                                                                           492
                                                                                                                                                                                                                                                                             AAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAA
                                                     CAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGG
                                                                  G---AGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTCATAGCCAGG
                                                                                                                             214 gaaaagaagatcaggttcagctaagactcaagtgcctgacctggaagctgatctccagg
                                                                                                                                                         AACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGCAGGAGATGG
                                                                                                                                                                                                            373 ACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTT
                             112 cacetectgagetgattgggcetatge----tggageeeeggtgatgaggag-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; NOVX; G-antigen; GAGE-like protein; interferon;
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                                                                                                                                                                                                                                                                                                                 493 TICICCCAATAAAGCITIACAGCCTICIGC 522
                                                                                                                                                                                                                                                                                                                                         453 atatogaaataaacttttgcagctttctcc 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0182724.
2000US-0182733.
2000US-0183896.
2000US-0184475.
2000US-0184497.
                                                                                                                                                                                                                                                                                                                                                                                                         AAD14981 standard; DNA; 475
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/*tag= b
/product=
361..475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV2 DNA.
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15-FEB-2000; 2
22-FEB-2000; 2
23-FEB-2000; 2
33-FEB-2000; 2
23-FEB-2000; 2
24-FEB-2000; 2
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5'UTR
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Gaps

22;

121; Indels

Pred. No. 4.4e-40; 0; Mismatches 121 Score 172.4;

Length 503;

ò 원 (first entry)

12-APR-2001

AAF68151;

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The present sequence is a human NOV2 DNA. The NOVX protein has homology with one of G-antigen (GAGE)-like protein, interferon, G-protein coupled receptor (GPCR), hepatocyte nuclear factor or mast cell protease. The NOVX is useful for treating or preventing a pathology associated with NOVX. It is also useful for determining the presence or amount of NOVX DNA in a sample, for identifying a potential therapeutic agent and in predisposition to a disease associated with altered levels of or predisposition to a disease associated with altered levels of NOVX. It is also useful for the diagnosis and treatment of proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g., cancer, immune disorders, heptic disorders, e.g., cirrhosis, viral infections, e.g., hepatitis, neuroolfactory system-related disorders, neurological disorders, e.g., Parkinson's disease, infertility, autoimmune diseases, arthritis, multiple sclerosis, allergies and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 GGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 CAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGATGGAC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 GCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGAG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                              Spytek KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 atcgaaaatgaaggagcacctgccgttcaagggcctgacatggaagcttttcaacaggaa
                                                                                                                                                                                                                                                                                                    Isolated novel polypeptides useful for diagnosis of and treating
                                                                                                                                                                                                                                                                                                                      cancer, infertility, autoimmune diseases, arthritis, multiple sclerosis, allergies, wound healing and hepatic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 475;
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                                                                                                                                                                                              Taupier RJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.2%; Score 130.4; DB 22; 64.9%; Pred. No. 6.8e-28; ive 0; Mismatches 116;
                                                                                                                                                                                          lev VT, Padigaru M, Tau
Spaderna SK, Boldog FL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 8; 140pp; English.
                                   18-SEP-2000; 2000US-0233105;
27-SEP-2000; 2000US-02350060
02-ANN-2001; 2001US-025414,
18-JAN-2001; 2001US-026454,
14-FEB-2001; 2001US-0783429.
 2000US-0197083
2000US-0224157
                                                                                                                                                                                        Tchernev VT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                      Malyankar UM, Tcherr
Majumder K, Guo X,
                                                                                                                                                     (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                               2001-514775/56
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                                                                                                                                                                                                                                                             P-PSDB; AAE08581
13-APR-2000;
10-AUG-2000;
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Best Local Simi
Matches 227;
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                                                                                                                                              agcaagacaaatgaagactgaaaccaagaacgttattcttaatctggaaatttgactgat 426
                                                                                                                                                                                                atgoccacttttgatctcactaaagtgctggaagcaggtgatgcgcaaccataggttca
                                                                                                                                                                                                                        435 AAGAAGACACGT----TGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATT
                                                                                                                                                                                                                                                                                         AAF68151 standard; cDNA; 399 BP
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The present invention describes immunogenic portions of lung tumourassociated proteins (1) and the nucleic acids (NAs) that encode them.

(1) have cytostatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumourassociated adjacenses associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (1). Additionally, the NAs may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA melocules may be administered to down regulate protein expression. The NA and complementary sequences and preventing their expression. The NA and complementary sequences and preventing their expression. The Associated protein and administrate the presence of similar NA sequences in samples, and hence which patients may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the protein. AAF68083 to AAF68878 and Control protein expression and activity of the protein are used in the exemplification of the proparation of the proparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                      Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 CCTGAAGAAGGGGAACCAGCAACTCAAGGATCCTGCAGCTGCTCAGGAG---GGA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                     Human lung tumour protein related nucleotide sequence SEQ ID NO:69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 20.1%; Score 108; DB 22; Length 3 Best Local Similarity 63.3%; Pred. No. 2e-21; Matches 214; Conservative 1; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 399 BP; 150 A; 87 C; 94 G; 67 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 173; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lodes MJ,
                                                                                                                                                                                                                                                                                                                                        99US-0419356.
99US-0466867.
99US-0476300.
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2000US-0546259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-071488/08
                                                                                                                                                                                                               WO200100828-A2.
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                    30-JUN-2000;
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10-APR-2000;
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30-DEC-1999;
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(CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                            377 GCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAA 436
                                                                                                       437 GAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTAAAATTCT 496
                                     125 gaagatcaggatacagctgagatcccagtgcgcgacatggaaggtgatctgcaagagctg 184
Kalos MD;
Carter D;
                   258 GAGGATGAGGAGCATCTGCAGGTCAAGGGCCGGAAGCCTGAAGCTCATAGCCAGGAACAG
                                                        GGTCACCCACAGACTGGGTGTGAGTGTGAAGAT-GGTCCTGATGGGCAGGAGATGGACCC
                                                                  Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                               CCCAATAAAGCTTTACAGCCTTCTGCAAAGAAAAAA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 387; 579pp; English.
                                                                                                                                                                                                                                                                                              Human prostate cDNA sequence #434
                                                                                                                                                                                                                                      BP
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2000US-0636215.
2000US-0651236.
2000US-0657279.
2000US-0679426.
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2000US-0570737.
2000US-0593793.
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                                                                                                                                                                                                                                                                           (first entry)
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13-JUN-2000;
27-JUN-2000;
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10-OCT-2000;
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the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGGAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCCGAAGCCTGAAGCTCATA 306
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olk JA, Skeiky YAW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aagttaaaaagaagacaagctgaagctacacacatggctgatgtcacattgaaaatgtga
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                                                                                                                                                                                                                                                                                                            Length 515;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harlocker SL, Jiang Y
Retter MW, Stolk JA,
                                                                                                                                                                                                                                Sequence 515 BP; 201 A; 81 C; 112 G; 118 T; 3 other;
                                                                                                                                                                                                                                                                                                               Score 101.6; DB 22;
Pred. No. 1.6e-19;
0; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate-specific cDNA sequence P1001C
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Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH93807 standard; cDNA; 515
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.2%;
Matches 221; Conservative
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                                                                                                                                     The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II), antibodies to (II), fusion proteins comprising (II), and isolated antibodies to (II) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can be used to monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH9344 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101.6; DB 22; Lcus-
Pred. No. 1.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 515 BP; 201 A; 81 C; 112 G; 118 T; 3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                         Claim 1; Page 385; 543pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.9%;
61.2%;
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                                                                      use in vaccines -
 WPI; 2001-425873/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Matches 221;
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The present invention describes an isolated polypeptide (PI) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (NI) encoding (PI). (PI) and (NI) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH8467 to AAH8513 and AAG99000 to AAG99077 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide and polypeptide sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                     Isolated polypeptide comprising at least an immunogenic portion or prostate-specific protein, useful in the diagnosis and therapy of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG
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                                                                                                                                                                                                                         Reed SG;
                                                                                                                                                                                                                       Harlocker SL, Jiang Y, Reed So
Day CH, Skeiky YAW, 'Wang A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 515 BP; 201 A; 81 C; 112 G; 118 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101.6; DB 22;
Pred. No. 1.6e-19;
0; Mismatches 125;
                                                                                                                                                                                                                     Dillon DC, Mitcham JL, Ha
MD, Retter MW, Stolk JA,
                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 285; 325pp; English
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ilarity 61.2%;
Conservative
                                                                                                   2000WO-US30904
                                                                                                                                                     99US-0443686
                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                       WPI; 2001-308785/32.
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Best Local Similarity
Matches 221; Conserv
                              WO200134802-A2.
Homo sapiens.
                                                                                                 09-NOV-2000;
                                                                                                                                   12-NOV-1999;
18-NOV-1999;
                                                                17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer
                                                                                                                                                                               Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
prostate cancer; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 515 BP; 201 A; 81 C; 112 G; 118 T; 3 other;
                                                                                                                                           Prostate tumour antigen cDNA sequence for P1001C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheever MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 267-268; 276pp; English
                                   AAH02872 standard; cDNA; 515 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ku J, Skeiky YAW, Reed SG,
                                                                                                                                                                                                                                                                                                                                        04-OCT-2000; 2000WO-US27464.
                                                                                                                                                                                                                                                                                                                                                                            99US-0157455.
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-245062/25.
                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                    WO200125272-A2
                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                            04-OCT-1999;
                                                                                                       14-JUN-2001
                                                                                                                                                                                                                                                                                                        12-APR-2001
                                                                     AAH02872;
15
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375 aagttaaaaagaagacaagctgaagctacacacatggctgatgtcacattgaaaatgtga 434
                                                                                                                                                                                                                                                                  Search completed: July 1, 2002, 07:11:23 Job time: 1919 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTGTTAAAAGAAGACACGTTGAAATGATGCA---GGCTGCTCCTATGTTGGAAATTTG- 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAGGAGGAGGAGGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 gacaagagagagaa-----ggaacacctccgatcgaagaacgtaaagtagaagtgatt 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 agaagactccacctaatcctaagcatgctaagactaaagaagcaggagatgggcagcat 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gccaggaaatggatctggaaaagactcggagtgagcgtggagatggctctgatgtaaaag 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; ' Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 18.9%; Score 101.6; DB 22; Length Best Local Similarity 61.2%; Pred. No. 1.6e-19; Matches 221; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
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 protein search, using sw model OM protein

1, 2002, 06:33:34 ; Search time 14.3 Seconds
(without alignments)
779.466 Million cell updates/sec Run on:

US-09-782-745-27 646

1 MSWRGRSTYRPRPRRYVEPP......DPPNPEEVKTPEEGEKQSQC 116 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

49123 hits satisfying chosen parameters: 283138 segs, 96089334 residues Total number of Searched:

length: 0 length: 116 sed Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

aggreen - pig (fr parathymosin - hum hypochetical prote prothymosin alpha prothymosin alpha hypothetical prote ribosomal protein 50s ribosomal prot pistil extensin-li troponin T, cardia procyclic acidic r prothymosin alpha prothymosin alpha hypothetical prote parathymosin rat procyclic acidic r GTP cyclohydrolage small proline-rich hypothetical prote myristylated tegum basic proline-rich hypothetical prote hypothetical prote BR6 protein - midg insulin-like growt Balbiani ring b ch hypothetical prote micro glutamic aci nonhistone chromos Description SUMMARIES \$55633 C38355 B72638 A55819 A437 A60674 S48790 FAUTPC S15073 TNRTA D72560 B31512 S54845 S78009 A32264 E70811 TNBOA1 T15547 C72637 I54187 S11755 R5HS2H F84266 405231 DB 116 102 114 80 83 102 109 Length Maton ဝေဆ Score 70 69.5 67.5 66.5 66.5 62.5 61.5 Result

lipoprotein [impor high mobility grou hypothetical prote	nonhistone chromos host specificity p aerC protein - Aer	hypothetical prote hypothetical prote nodulin - alfalfa	hypothetical prote capsid assembly pr hypothetical prote	hypothetical prote sperm histone P2 p nonhistone chromos von Hippel Lindau
C90564 JC2232 T22131	A33310 S07520 S03097	S77141 AE3247 S04554	T35249 VHBPP4 A64563	T04512 HSHUP2 S08180 I38926
000	200	000	212	7777
101 109 87	100 106 61	74 94 97	109	99 102 103 59
1.00	0.00	& & & &		8.7 8.7 8.7 8.7
58.5 58.5	58 57.5 57	57 57 57	57 57 57	56.5 56.5 56.5 56.5
30 32	3 3 33 5 4 3	36 37 38	39 40 11	4 4 4 4 2 6 4 3

## ALIGNMENTS

 RESULT 1
urbo micro glutamic acid-rich protein – bovine N;Alternate names: neurofilament triplet L protein (fragment)
C;Species: Bos primigenius taurus (cattle) C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 22-Nov-1996
 C.Accession: A0290 R.Isobe, T.; Okuyama, T. FEBS Lett. 182, 389-392, 1985
A; Title: Brain micro glutamic acid-rich protein is the C-terminal endpiece of the A; Reference number: A02964; MUID:85154567
 A;Accession: A02964 A;Molecule type: protein
A; Residues: 1-82 <150>
C;Comment: The similarity of this sequence to part of the neurofilament triplet L
f the L protein.
C.Comment. Although there are, as yet, no known biological functions ascribed to
 C.Superfamily: cytoskeletal Keratin
C; Keywords: brain; coiled coil; cytosol; intermediate filament
F;I-84/Domain: neuroritament triplet L protein tail subdomain D (irayment) sator
 12.0%;
Best Local Similarity 28:9%; Fred. No. 17; Matches 24; Conservative 15; Mismatches 27; Indels 17; Gaps 4;
 QY 36 EPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPD 92
 Db 2 EPPSEGEAEEEEKEKEEAEAEEEGAQEEEAEAAKEDAEEAKEEEGGE 52
 QY 93 GQEMDPPNPEEVKTPEEGEKQSQ 115
Db 53 GEEAEETKEABEEERKDE 70

## ~ RESULT

S55633

Myristylated tegument protein 38 - equine herpesvirus 2

myristylated tegument protein 38 - equine herpesvirus 2

myristylated tegument protein 38 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Accession: S55633

G;Accession: S55633

Myrielle: The DNA sequence\_revision 03-Nov-1995 #text\_change 08-Oct-1999

C;Accession: S55633

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S5594; MUID:95302501

A;Accession: S55633

A;Accession: S55633

A;Accession: S55633

A;Accession: S55633

A;Accession: S56633

A;Accession: S56634

A;Accession: S56634

A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13826.1; PID:g695211

62

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nonhistone chromosomal protein CHMG-I - midge (Chironomus tentans)
N.Alternate names: high mobility group protein I/Y homolog
C.Species: Chironomus tentans
C.Species: Asra-1995 #sequence_revision 05-Apr-1995 #text_change 21-Jul-2000
C.Accession: A55819; 847253; 847252
R.Ciaus, P.; Schulze, E.; Wisinawski, J.R.
J. Biol. Chem. 269, 33042-33048, 1994
A;Title: Insect proteins homologous to mammalian high mobility group proteins I, A;Reference number: A55819; MUID:95105193
A;Accession: A55819
A;Molecule type: mRNA
A;Residues: 1-99 CCLDA
A;Cross-references: EMBL:236898; NID:9534932; PIDN:CAA85365.1; PID:9534933
A;Experimental source: clone pCW126
R;Claus, P.; Schulze, E.; Wisniewski, J.R.
Submitted to the EMBL Data Library, August 1994
A;Description: Insect proteins homologous to mammalian high mobility group proteins A;Accession: S47253
A;Molecule type: DNA
A;Residues: 1-91, A',93-99 CCLZ>
A;Cross-references: EMBL:236897; NID:9534886; PID:9534887
A;Experimental source: clone pCWG106
C;Genetics:
C;Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: EMBL:AC004625; NID:g3241939; PID:g3241940
A.Experimental source: cultivar Columbia
Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein At2g41420 [imported] - Arabidopsis thaliana NiAlternate names: hypothetical protein T26J13.1 C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001 C.Accession: T02437; E84841 F.Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998 A.Description: Arabidopsis thaliana chromosome II BAC 726J13 genomic sequence. A.Reference number: 214673
          5 KHEPNPQGEGED-GPEGARGEEPGHPAQDDGEARRGAEAA-GPGHEALLPRQVREMRGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQ-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Note: suggested by Southern blot analysis in Ref. C. Keywords: chromosomal protein; DNA binding F. F. 13. Region: DNA-binding motif (K. R-G-R-G-R-P) F. 55-60/Region: DNA-binding motif (K. R-G-R-G-R-P) F. 75-80/Region: DNA-binding motif (K. R-G-R-G-R-P)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 69.5; D 24.7%; Pred. No. 77; iive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || | : :| | : | | :|::
PKRPASGKGRGRPAKNAKKVDDADTEEVN 96
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A;Molecule type: DNA
A;Residues: 1-98 <ROU>
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Best Local Similarity
Matches 22; Conserv
                                                                           109 EGEKQS 114
                                                                                                                                        63 QPEEEA 68
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Accession: B2638
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Rase. 6, 83-101, 1999
A;Reference number: A72450; MUID:99310339
A;Reference number: A72450; MUID:99310339
A;Recession: B72638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 < KAW>
A;Residues: 1-101 < KAW>
A;Residues: 1-101 < KAW>
A;Experimental source: strain K1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G
   EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 12-Apr-1995
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 12-Apr-1995
C;Cocsasion: C38355
B;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A;Title: Basic proline-rich proteins from human parotid saliva: relationships of the A;Accession: C38355
A;Status: preliminary
A;Accession: C38355
A;Status: proline-rich protein
A;Residues: 1-76 cKAU>
C;Superfamily: proline-rich protein
                                                                                                                                                                       ά,
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                                                                                                                                                                           Gaps
                                                                                                                                                                                                                       36 EPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQE 95
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                      91;
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                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 76;
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                                                                                                      Length
                                                                                                                                                                38;
A; Note: the nucleotide sequence was submitted to the
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Llarity 25.8%; Pred. No. 72;
Conservative 16; Mismatches 3
                                                                                                      DB
                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _
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                                                                                               Score 74.5; |
Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.0%; Score 71; Best Local Similarity 27.4%; Pred. No. 4 Matches 20; Conservative 9; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              basic proline-rich peptide II-2 - human
                                                                                               11.5%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
-
                                                                                                                                                                                                                                                                                                                                                         96 MDPPNPEEVKTPEEGEKQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                       GREPOPEVKTTPYPKRKK 83
                                                          Query Match
Best Local Similarity 30.0.
-hac 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 NPEEVKTPEEGEK 112
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Best Local Similarity
Matches 17; Conserv
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A55819 to be single copy gen:

3;

Gaps

Length 99;

2;

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C; Superfamily: insulin receptor; protein kinase homology C; Keywords: ATP; growth factor receptor; membrane protein
                                                                                                                                                                                                                                                                                                                 9 YRPRPRRYVEPP--EMIGPMRPEQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%;
28.0%;
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ilarity 34.1%;
Conservative 6
                                                                                                                                                          10.3%;
28.4%;
                                                                                                                                                          Query Match 10.3%
Best Local Similarity 28.4%
Matches 27; Conservative
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Best Local Similarity 28.0
Matches 21; Conservative
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Best Local Similarity
Matches 14; Conserv
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S48790
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C; Species: Mus musculus (house mouse)
C; Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 23-May-1997
C; Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 23-May-1997
C; Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 23-May-1997
C; Accession: A60674
R; Telford, N.A.: Hogan, A.; Franz, C.R.: Schultz, G.A.
MOI. Reprod. Dev. 27, 81-92, 1990
A; Title: Expression of genes for insulin and insulin-like growth factors and receptors A; Reference number: A60674; MUID:91064061
A; Reference number: A60674
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Mesidues: 1-102 <TEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A43732

BR6 protein - midge (Chironomus tentans) (fragments)

BR6 protein - midge (Chironomus tentans)

C;Species: Chironomus tentans

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 17-Mar-1999

C;Accession: A43732

R;Lendahl, U.; Wieslander, L.

Cell 36, 1027-1034, 1984

A;Title: Balbiani ring 6 gene in Chironomus tentans: a diverged member of the Balbiani

A;Reference number: A43732

A;Status: preliminary

A;Status: preliminary

A;Status: preliminary

A;Status: Dreliminary

A;Residues: 1799 <LEN>

A;Residues: 1790 <LEN>

A;Residues: 1790 <LEN>

A;Residues: 1700 ×LEN>

A;Residues: 
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487
A.Rocession: E84841
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-98 <STO
A.Gross-references: GB:AE002093; NID:g3241940; PIDN:AAC23727.1; GSPDB:GN00139
C.Genetics:
A.Gene: T265133.1; At2941420
A.Map position: 2
A.Introns: 16/1: 84/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEEGEPATORODPAAAQEGEDEGASAGOGPKPEAHSOE----OGHPOTGCECEDGPDGQE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 67.5; DB 2; 129.1%; Pred. No. 1.1e+02; ive 10; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 66.5; DB 2;
Pred. No. 1e+02;
9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.3%;
Best Local Similarity 28.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 MDPPNPEEVKTPEEGEKQS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: ::||
59 -PPYAPQYPPPPQHQQQQS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 EAHSQEQGHPQTGCEC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 RCDNENRRFDARRCEC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
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Procyclic acidic repetitive protein precursor (clone pAP3) - Trypanosoma brucel N;Alternate names: procyclin (c;Species: Trypanosoma brucei brucei Trypanosoma brucei brucei Species: Trypanosoma brucei brucei (c;Species: 31-bec-1991 #sequence_revision 31-bec-1991 #text_change 22-Jun-1999 (c;Accession: S14896; S06170 R;Koenig, E.; Delius, H.; Carrington, M.; Williams, R.O.; Roditi, I. Nucleic Acids Res. 17, 8727-8739, 1989 A;Tile: Duplication and transcription of procyclin genes in Trypanosoma brucei. A;Reference number: S14896; MUID:90067841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ProA
C;Superfamily: procyclic acidic repetitive protein
C;Superfamily: procyclic acidic repeat
F;1.27/Domain: signal sequence #status predicted <SIG>
F;28-115/Product: procyclic acidic repetitive protein #status predicted <MAT>
F;63-92/Region: 2-residue repeats (E-P)
F;56/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unional T, cardiac muscle (clone HTNT3) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: $48790
B;Farza, H.
Submitted to the EMBL Data Library, June 1994
A;Reference number: $48790
A;Reference number: $48790
A;Reference number: $48790
A;Reference number: $48790
A;Residues: 1-72 <FRR>
A;Residues: 1-72 <FRR>
A;Residues: 1-72 <FRR>
A;Residues: 1-72 <FRR>
C;Superfemnily: troponin T
C;Superfemnily: troponin T
C;Keywords: cardiac muscle; heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                             2 YNPK----IRPSFLEIIGSIKDEMEPSFQEVSFYYSEENKPPEPEELEMELE-mEPENIG 56
                                                                                                                          ----FSDEVEPATPEEGEPATQRODPAAAQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-115 <KOE>
A;Cross-references: EMBL:X16015; NID:g10512; PIDN:CAA34147.1; PID:g10513
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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Length 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.5; DB 1;
Pred. No. 2.9e+02;
7; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 DEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEA 73
; Score 66.5; DB 2;
; Pred. No. 1.3e+02;
13; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                    57 EGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
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57 ELPLDPRSQSSLPLPERHS---GH-----KAENGP
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A; Title: The MYC protein activates transcription of the alpha-prothymosin gene.
A; Reference number: I53187; MUID:91114696
A; Reference number: I53187
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-112_CELL.
A; Cross-references: EMBL:X55326; NID:957661; PIDN:CAA39028.1; PID:957662
A; Experimental source: cell line RATIA
A; Rote: in GenBank entry RRPROTHYO, release 113.0, the source is designated as F; RHarites, A.A.; Blacher, R.; Stein, S.; Caldarella, J.; Horecker, B.L.
Proc. Natl. Acad. Sci. U.S.A. 82, 343-346, 1985
A; Ritle: Primary structure of rat thymus prothymosin alpha.
A; Reference number: A01519; MUID:85113197
A; Rocession: A01519
A; Molecule type: protein
A; Residues: 2-61, G', 63-64, BGGZZZZZZZZZZNV, 77-112 <HARL>
A; Note: it is possible that both Asp and Asn are present at positions 29 and 36
B; Haritos, A.A.; Goodall, G.J.; Horecker, B.L.
Proc. Natl. Acad. Sci. U.S.A. 81, 1008-1011, 1984
A; Title: Prothymosin alpha: isolation and properties of the major immunoreactive A; Reference number: A20738; MUID:84144830
A; Molecule type: Prothymosin alpha: isolation and properties of the major immunoreactive A; Reference number: A20738; MUID:84144830
A; Molecule type: Prothymosin alpha: isolation and properties of the major immunoreactive A; Reference number: A20738; MUID:84144830
A; Molecule type: Prothymosin alpha: A20738; MUID:84144830
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A;Residues: 2-31 (EIRA2)
FEBS Lett. 277, 257-260, 1990
A;Title: Identification of a low-M(r) acidic nuclear protein as prothymosin alph
A;Reference number: S13014; MUID:91099511
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A.Molecule type: protein
A.Residues: 2-112 <PAL>
C:Comment: This highly acidic protein was originally studied as a putative thymi
arent function may not be physiological. The native protein is expressed in a bro
precise role is not yet known.
C:Superfamily: prothymosin alpha
C:Reywords: blocked amino end; nucleus; phosphoprotein
C:Superfamily: prothymosin alpha #status experimental <MAT>
F:2-112/Product: prothymosin alpha #status experimental <TMAA
F:2-29/Product: thymosin alpha-1 #status experimental <TMAA
F:2-29/Product: thymosin alpha-1 #status form) (probably acetylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D72560
hypothetical protein APE1766 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72560
B;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, Kawa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 81-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 VEPATPEGGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQ
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llarity 24.7%; Pred. No. 3.1e+02;
Conservative 13; Mismatches 43.
              A; Reference number: A37401; MUID:91031267
A; Accession: A37401
A; Molecule type: mRNA
A; Residues: 1-63, K', 65-67, K', 69-83 <OIK>
A; Cross-references: GB:M60664
A; Note: 64-Glu and 68-Glu were also found
EX; Eilers, M.; Schirm, 53; Bishop, J.M.
EMBO J. 10, 133-141, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 EMDPPNPEEVKTPEEGE 111
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prothymosin alpha - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S15073; S12883; S06666
R;Schmidt, G; Werner, D2883; S06666
B;Schmidt, G; Werner, D2888, 442-444, 1991
B;Schmidt, G; Werner, D2889, 452-444, 1991
A;Title: Nucleotide sequence of the murine prothymosin alpha cDNA and its deduced primar A;Title: Nucleotide sequence of the murine prothymosin alpha cDNA and its deduced primar A;Title: Nucleotide sequence of the murine prothymosin alpha cDNA and its deduced primar A;Teterence number: S15073
A;Tetus: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <SCH>A;CRSCHS = MRNA
A;Residues: 1-111 <SCH>A;CRSCHS = MRNA
A;Title: PENS = MRNA
A;Titl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Title: Depression of prothymosin-alpha production in murine thymus correlates with sta A.Title: Depression of Prothymosin-alpha production in murine thymus correlates with sta A.Reference number: S12883; MUID:91032153
A.Reference number: S12883; MUID:91032153
A.Status: preliminary
A.Molecule type: protein
A.Residues: 2-106, K'.107-111 <LOW>
FEBS Lett. 257, 247-250, 1989
A.Title: Prothymosin alpha is an evolutionary conserved protein covalently linked to a s A.Reference number: S06666; MUID:90060328
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1987 **Bequence_revision 02-Dec-1994 **text_change 16-Jun-2000
C:Date: 30-Jun-1987 **Bequence_revision 02-Dec-1994 **text_change 16-Jun-2000
C:Accession: A32265; A37401; I53187; A01519; A20738; S13014
R:Frangou-Lazaridis, M.; Clinton, M.; Goodall, G.J.; Horecker, B.L.
Arch: Biochem. Biochhymys. 263, 305-310, 1988
Arch: Biochem. Biochhymys. 263, 305-310, 1988
Arth: Prothymosin alpha-and parathymosin: amino acid sequences deduced from the clone A;Reference number: A32265; MUID:88239673
A;Recession: A32265
A;Mocleule type: mRNA
A;Residues: 1-112 <FRA>
A;Ressidues: 1-112 <FRA>
A;Ressidues: 1-112 <FRA>
A;Ressidues: 1-112 <FRA>
A;Ressidues: 1-112 <FRA>
A;Chxawa, M.; Dargan, C.; Ny, T.; Hsueh, A.J.W.
Endocrinology 127, 2350-2356, 1990
A;Title: Expression of gonadotropin-releasing hormone and prothymosin-alpha messenger ri
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                                                         QGPKPEAHSQEQGHPQTGCECEDGPDGQE
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A;Residues: 16-19;23-68;91-100,'E',102-103 <MAK>
C:Superfamily: prothymosin alpha
C:Keywords: nucleus; phosphoprotein
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Keywords: nucleus; phosphoprotein
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                                                                                                                                                                                     MDPPNPEEVKTPEEG 110
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    AAAQEG-EDEGASAG-
53
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A;Residues: 2,'KSE',6-31 <HAR>
C;Superfamily: prothymosin alpha
C;Keywords: acetylated amino end; zinc
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experiment.
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C; Date: 28-Feb-1990 #sequence_revision 02-Dec-1994 #text_change 16-Jul-1999
C; Date: 28-Feb-1990
C; Date: 28-Feb
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R'Frangou-Lazaridis, M.; Clinton, M.; Goodall, G.J.; Horecker, B.L.

R'Frangou-Lazaridis, M.; Clinton, M.; Goodall, G.J.; Horecker, B.L.

A'Title: Biochem. Biophys. 263, 305-310, 1988

A'Freference number: A32265; MUID:88239673

A'Reference number: A32265

A'Status: Brainflaary

A'Molecule type: mRNA

A'Residues: 23-102 CFRAA

A'Residues: 23-102 CFRAA

A'Residues: 23-102 CFRAA

A'Cross-references: GB:M33025; NID:9206032; PIDN:AAA1810.1; PID:9206033

R'Komlyama, T.; Pan, L.X.; Haritos, A.A.; Wideman, J.W.; Pan, Y.C.E.; Chang, M.; Rogers, A'Reference number: A05095; MUID:86149281
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A;Experimental source: strain K1
C;Genetics:
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A; Residues: 2-102 VEAN>
R; Wellner, D.; Panneerselvam, C.; Horecker, B.L.
Proc. Natl. Acad. Sci. U.S.A. 87, 1947-1949, 1990
A; Title: Sequencing of peptides and proteins with blocked N-terminal amino acids: N-acet
A; Reference number: A35060; MUID:90175413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: 11K zinc-binding protein; phosphofructokinase-1-inactivating protein
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                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
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Pred. No. 3.2e+02;
7; Mismatches 41;
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Best Local Similarity 24.4%;
Matches 22; Conservative
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                                                                                                                     1-116 <KAW>
                                                                                    A; Molecule type: DNA
    A; Accession: D72560
A; Status: prelimina
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A)Cross references: GB:M25787; NID:g341399; PIDN:AAA53283.1; PID:g576546
R;Vijayasarathy, S.; Ernest, I.; Itzhaki, J.; Sherman, D.; Mowatt, M.R.; Michels, submitted to the EMBL Data Library, April 1990
A;Description: The genes encoding fructose bisphosphate aldolase in trypanosoma b A;Reference number: S21538
A;Accession: S21539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Trypanosoma brucei
C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 13-Aug-1999
C; Accession: 330229; S21539
R; Mowatt, M.R.; Wisdom, G.S.; Clayton, C.E.
Mol. Cell. Biol. 9, 1332-1335, 1989
A; Title: Variation of tandem repeats in the developmentally regulated procyclic
A; Reference number: A30229; MuID:89261740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 DESASNVIVKGGKCKEREDGPEEPEETGPEETGPE-ETGPEETGPEET-GPEETE 86
                                                                                                                                   ---DGQEM 96
                                                                                                                                                                                                 39 BEEENGAEEEEEETAEDGEDD----DEGDEEDEEEE-----EEDEGPVRKRTAEEE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X52584; NID:g10480; PIDN:CAA36814.1; PID:g10481
C;Superfamily: procyclic acidic repetitive protein
Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                procyclic acidic repetitive protein A-alpha – Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.4%; Score 61; DB 2; Length 114; illarity 34.4%; Pred. No. 3.7e+02; Conservative 8; Mismatches 24; Indels
                                                                     Indels
                                                                                                                                      41 EEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGP
9.5%; Score 61.5; DB 2;
25.7%; Pred. No. 3.1e+02;
tive 15; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1, 2002, 06:37:04
                                                                     Conservative
                                                                                                                                                                                                                                                                                                            | :|: || | |
DEADPKROKT-ENG
                                                                                                                                                                                                                                                                   DPPNPEEVKTPEEG
                                  Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-114 <MOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-114 <VIJ>
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Job time: 210 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 1, 2002, 06:36:39 ; Search time 12.61 Seconds (without alignments) 356.183 Million cell updates/sec Run on:

US-09-782-745-27 646

1 MSWRGRSTYRPRPRRYVEPP......DPPNPEEVKTPEEGEKQSQC 116 Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

16058 Total number of hits satisfying chosen parameters:

length: 0 length: 116 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		dР			SUMMARIES		
Result No.	Score	Query Match	Query Match Length	DB	ID	Description	
-	646	100.		-	GGE2_HUMAN	Q13066 homo sapien	
7	120	18.	102	7	GGC1_HUMAN	homo	
m	72.5	11.	85	7	MRKD_RAT	rattu	
4	70.5		96	7	PRP5_HUMAN	P04281 homo sapien	
S	62.5	o,	61	Т	PRPE_HUMAN	рошо	
9	62.5	σ.	115	Т	PARX_TRYBB	trypa	
7	62	ο,	110	П	THYA_MOUSE.	_	
æ	62		111	7	THYA_RAT	P06302 rattus norv	
σ	61.5	9.5		7	THYP_RAT	P04550 rattus norv	
10	61	9.4		П	MEA1_PIG	Q95313 sus scrofa	
11	61	9.4		Н	PARA_TRYBB	P18764 trypanosoma	
12	60.5	9.4		~	PGCA_PIG		
13	60.5	9.4		Н	THYP_HUMAN	P20962 homo sapien	
14	59.5	9.5		٦	THYA_BOVIN	bos t	
15	59.5	9.5		Н	RL12_HALHA	P05768 halobacteri	
16	58.5	9.1		7	CORA_HUMAN	P35321 homo sapien	
17		9.1		Н	HMGC_HUMAN	homo	
18	S	9.0		7	HG14_HUMAN	homo	
19	57.5	8.9		7	THYP_BOVIN	P08814 bos taurus	
20	57.5	8.0		-	VHSB_BPT3	P20322 bacteriopha	
21	57	8.8		Н	AERC_AERSO	-	
22	57	8.8		Н	NO75_MEDSA		
23	in	8.8		-	VG31_BPT4		
24		8.7		7	HG14_CHICK		
22	56.5	8.7		_	HSP2_HUMAN		
56		8.7		٦	THYA_HUMAN		
27	S	8.7		~	ET3_RABIT	oryct	
28	55.5	8.6		-	DAP1_HUMAN	P51397 homo sapien	
29		8.6		Н	HSP2_MACMU	_	
30		8.6		٦	HSP2_MACNE	P35298 macaca neme	
31		8.5		H	MT21_ORYSA	_	
32	٠	8.4	88	_	CORB_HUMAN	P22528 homo sapien	
33	54.5	8.4	88	7	CORN_MACMU	~	

95 1 HMGY_MOUSE P17095 mus musculu P02316 bos taurus P02316 bos taurus P02316 bos taurus P12902 gallus gall P05918 bos taurus P12902 gallus gall P05918 bos taurus P05918 bos sapien P071 DPD4_HUMAN P05918 bos sapien P071 COLL_HOYS7 P09944 hirudo medi P0502 bom Sapien P0502 bom Sapien P0502 bom Sapien P0502 bom Sapien P0503	ALIGNMENTS ARD; PRT; 116 AA.	36, Created) 36, Last sequence update) 39, Last annotation update) antigen 2).	Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.	PubWed=7544395; Peeters O., de Backer O., Gaugler B., Lucas S.,	coding for an antigen recognized by autolion a human melanoma."; 18(1995). RECOGNIZER ON MELANOMA BY AUTOLOGOUS CYTC	TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR TISSUES BUT NOT IN NORMAL TISSUES, EXCEPT TESTIS. SIMILARITY: BELONGS TO THE GAGE FAMILY.
88.4 88.4 88.3 88.3 88.3 1000 88.3 1000 88.2 1000 88.1 1000 88.1 1000 88.1 1000 88.1 1000 88.3 88.3	STANDARD;	36, 36, 39, anti	~		of genes ymphocytes 182:689-69 ANTIGEN,	TISSUE SPECIFICITY: EXF NOT IN NORMAL TISSUES, SIMILARITY: BELONGS TO
44	T 1 HUMAN GGEZ_HUMAN	Q13066; 15-JUL-1998 (Rel. 15-JUL-1998 (Rel. 30-MAY-2000 (Rel. GAGE-2 protein (G GAGE2.	sapiens yota; Me lia; Eut TaxID=96	SEQUENCE FROM N.A. TISSUE=Melanoma; MEDLINE=95378788; van den Eynde B.,	"A new family of genes cytolytic T lymphocytes J. Exp. Med. 182:689-69 -!- FUNCTION: ANTIGEN, T LYMPHOCYTES.	-!- TISSUE SPE NOT IN NOF -!- SIMILARITA
W W W W W W W A A A A A A A A A A A A A	SUL E2_	S D D D D D D D D D D D D D D D D D D D				8888

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). ö 0; Gaps Length 116; Indels DD305D5CA29AF19A CRC64; Ouery Match 100.0%; Score 646; DB 1; Best Local Similarity 100.0%; Pred. No. 3.8e-38; Matches 116; Conservative 0; Mismatches 0; EMBL; U19143; AAA82745.1; -. MIM; 604244; -. SUULIGENE family. SEQUENCE 116 AA; 12786 MW;  $\begin{array}{c} \mathbb{Z} \\ \mathbb{$ 

9 1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGED 60 g ò

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Rozengurt E.;
                                                                                                      bovine brain.
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NON_CONS
SEQUENCE
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SEQUENCE
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PRP5_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratius norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATGRQDPAAAQEGED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSARVESERGRGDGQ-EAPDVVA------FVAPGESQQEEPPTDNQDIEPCQ--ER 48
                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: UNKNOWN.
-!- FUNCTION: UNKNOWN.
-!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NORMAL MALE AND FEMALE REPERDUDCHIVE TISSUES, PROSTATE, TESTIS, FALLOPIAN TUBE, UTERUS, AND PLACENTA, AS WELL AS IN PROSTATE CANCER, TESTICULAR CANCER, AND UTERINE CANCER.
-!- SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                  "PAGE-1, an X chromosome-linked GAGE-like gene that is expressed in
                                                                                                                                                                                                                                                                                             Strom T.M., Nyakatura G., Hellebrand H., Drescher B., Rosenthal A.,
                                                                               4
                                                                                                                               Euteleostomi;
                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
G antigen family C 1 protein (Prostate-associated gene protein (PAGE-4) (PAGE-1) (JM27) (GAGE-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQ 113
                                                                                                                                                                                                        Brinkmann U., Vasmatzis G., Lee B., Yerushalmi N., Essand M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.6%; Score 120; DB 1; Length 102; 34.5%; Pred. No. 0.02; ive 10; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                      Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRKD_RAT STANDARD; PRT; 85 AA.
P20468;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Protein kinase C substrate 80 KDa protein (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 AA; 11153 MW; CE5D07AFBF73301B CRC64;
                                                                                                                                                                                                                                              normal and neoplastic prostate, testis, and uterus.";
Proc. Natl. Acad. Sci. U.S.A. 95:10757-10762(1998).
                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
             102 AA.
             PRT;
                                                                                                                                                                              EMBL; AF275258; AAF88037.1; -. EMBL; AJ005894; CAA06751.1; -.
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             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300287;
          GGC1_HUMAN
O60829;
                                                                                                                                                                                                                                                                                                         Meindl A.;
                                                                                                                                                                                                                     Pastan I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
GGC1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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PITS, A03293; PIHUBL.
Phosphorylation; Repeat; Parotid gland; Saliva.
MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 8 PHOSPHORYLATION.
                                                                                  kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EAAAERPGEAAVASSPGXAAAAAGGDAAAAPGEQAGGAGAGGAEGEEKAEE---PAPGA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 EPATPEEGEPATQRQ-----DPAAAQEGEDEGASAGQGPKPEAHSQEQHPQTGC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                  kDa protein kinase
kDa substrate from
                                                                                                                                                                 -i- FUNCTION: CELLULAR SUBSTRATE FOR PROTEIN KINASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86243355; PubMed-3521730;

Kauffman D., Hofmann T., Bennick A., Keller P.;

"Basic proline-rich proteins from human parotid saliva: complete covalent structures of proteins IB-1 and IB-6.";

Biochemistry 25:2387-2392(1986).

1- DOMAIN: CONTAINS 21-RESIDUE REPEATS, TWO OF WHICH HAVE INTERNAL 7-RESIDUE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                            Brooks S.,
                                                                                                                                                                                                                                                                                                                                                                                                                Length 85;

    Length 96;

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21
50
74
7593 MW, 39501D788C12E268 CRC64;
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                                                                                80
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                              "Internal amino acid sequence analysis of the substrate from rat brain: relationship to the bovine brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
10-CT-1994 (Rel. 30, Last annotation update)
Basic proline-rich peptide IB-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 70.5; DB
Pred. No. 43;
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
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TISSUE-Brain;
MEDLINE=90005952; PubMed=2676596;
Erusalimsky J.D., Morris C., Perks K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 ECEDGPD--GQEMDPPNPEEVKTP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 255:149-153(1989).
                                                                                                                                                                                                                                                                                                                                                                                                              11.2%;
27.4%;
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Best Local Similarity 27.7%;
Matches 26; Conservative
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35
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77
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les 23; Conserv
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20
49
73
85 AA;
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                                                                                                                                                                                                                                               Phosphorylation.
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01-MAY-1992
01-MAY-1992
01-MAR-2002
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CARBOHYD
SEQUENCE
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PROPEP
                                                                                                  brucei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Saliva;
MEDLINE-8300719; PubMed-7118863;
ISEMURA S., Saitch E., Sanada K.;
"Fractionation and characterization of basic proline-rich peptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=5702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----QGPPPQGGNRPQ 39
T | | | : | : | | | : | : | EDVSQEESPEILAGNPQGAPPQGGNKPQGPPSPPGKPQGPPPGGGNQPQGPPPP-GKPQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kauffman D., Wong R., Bennick A., Keller P.;
"Basic proline-rich proteins from human parotid saliva: complete covatent Structure of protein IB-9 and partial structure of protein IB-6, members of a polymorphic pair.";
Biochemistry 21:6558-6562(1982).
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Procyclin) (PARP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan parotid saliva and the amino acid sequence of proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Blochem. 91:2067-2075(1982).
-1- MISCELLANEOUS: PEPTIDES IB-9 AND P-E ARE THE SAME PEPTIDE.
PIR; A03292; PIHUB9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.7%; Score 62.5; DB 1; Length 61; 23.6%; Pred. No. 1e+02; Live 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPROXIMATE.
APPROXIMATE.
APPROXIMATE.
F883F78617E05327 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
Procyclic form specific polypeptide precursor
                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) Basic proline-rich peptide P-E (IB-9).
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                                                         79 GHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEK 112
                                                                                                  64 GPPPQGGNKPQGP-----PPPGKPQGPPPQGDK 91
                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Parotid gland; Saliva
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6024 MW;
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                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
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. AA;
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Matches 21;
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P14043;
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ID PARX_T
AC P14043
DT 01-APR
DT 15-UIL
DE PPCCYC
GN PROA...
OS Trypan
OX CL EUKATY
RN [1]
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PRPE_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                         GPI-anchor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt G., Werner D.; "Nucleotide sequence of the murine prothymosin alpha cDNA and its deduced primary and secondary protein structure."; Biochim. Biophys. Acta 1088:442-444(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AAAAEGPEDKGLTKGGKGKGEKGTKVGADDTNGTDPDPEPEPEPEPEPEPEPEPEPE---
                                                                                                                                                               Nucleic Acids Res. 17:8727-8739(1989).
-!- FUNCTION: MAJOR SURFACE ANTIGEN OF PROCYCLIC FORMS.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
-!- DEVELOPMENTAL STAGE: EXPRESSED ONLY AT A CERTAIN STAGE DURING
DIFFERENTIATION IN THE INSECT VECTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Mus
SEQUENCE FROM N.A.
STRAIN-227(ILTAT1);
MEDLINE-906078411; PubMed-2573878;
MEDLINE-906078411; PubMed-2573878;
Koenig E., Delius H., Carrington M., Williams R.O., Roditi I.;
"Duplication and transcription of procyclin genes in Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROCYCLIC FORM SPECIFIC POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 x 2 AA TANDEM REPEATS OF [DE]-P. N-LINKED (GLCNAC. . .) (POTENTIAL). 6D39F0731CF0509E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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LOW T.L.K., Pan T.L., Lin Y.S.;
"Depression of prothymosin alpha production in murine thymus
correlates with staphylococcal enterotoxin-B-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62.5; DB 1; Length 115;
Pred. No. 1.8e+02;
7; Mismatches 24; Indels 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 41, Last annotation update)
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115
92
17
56 N-
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Best Local Similarity 20...
Loc 21; Conservative
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59
56
115 AA;
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EMBO J. 10:133-141(1991).
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                                                    PRELIMINARY
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PEPTIDE
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P04550;
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THYP_RAT
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                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wolfied by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                           Makarova T., Grebenshikov N., Egorov C., Vartapetian A., Bogdanov A., Prothymosin alpha is an evolutionary conserved protein covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 257:247-250(1989).
-!- FUNCTION: Prothymosin alpha may mediate immune function by conferring resistance to certain opportunistic infections.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- PIM: COVALENTLY LINKED TO A SMALL RNA OF ABOUT 20 NUCLEOTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88239673; PubMed-3377505;
Frangou-Lazaridis M., Clinton M., Goodall G.J., Horecker B.L.;
"Prothymosin alpha and parathymosin: amino acid sequences deduced
from the cloned rat spleen CDNAs.";
Arch. Bloochem. Blophys. 263:305-310(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.6%; Score 62; DB 1; Length 110; 24.7%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THYMOSIN ALPHA.

ACETYLATION (BY SIMILARITY).

ASP/GLU-RICH (ACIDIC).

K -> KK (IN REF. 2).

AF321A324731826F CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prothymosin alpha.
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  OF 14-17; 21-67 AND 90-102.
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                      MEDLINE=90060328; PubMed=2479575;
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INIT_MET 0 0 0
PEPTIDE 1 28
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105
                                                                                       linked to a small RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THYA_RAT
P06302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                             FEBS Lett. 277:257-260(1990).
-!- FUNCTION: Prothymosin alpha may mediate immune function by conferring resistance to certain opportunistic infections.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- PIM: Covalently linked to a small RNA of about 20 nucleotides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 VEEA - - ENGRDAPANGNAQNEENGEQEADNEVDEEEEEGGEEEEEEEGGGEEEDGGEEDGDEDE 80
                                                                                                                                                 PARTIAL SEQUENCE:
MEDIATR=-9109511; PubMed=2269362;
MEDIATR=-9109511; Linnala-Kankkunen A.;
"identification of a low-Mr acidic nuclear protein as prothymosin
                                                    Horecker B.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 VEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39FF33AADDE5A182 CRC64;
                MEDLINE-85113197; PubMed-385555; Haritos A.A., Blacher K., Stein S., Caldarella J., Hor Primary structure of rat thymus prothymosin alpha."; Proc. Natl. Acad. Sci. U.S.A. 82:843-346(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLATION.
ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.6%; Score 62; DB 1; 7 24.7%; Pred. No. 1.9e+02; 1ive 13; Mismatches 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
141, Last annotation update)
Parathymosin (Zinc-binding 11.5 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THYMOSIN ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AA.
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MEDLINE-89338759; PubMed=2759245;
Trompeter H.-I., Brand I.A., Soeling H.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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PIR; A32265, A32265, PIR; S13014; S13014; B13014.
Acetylation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12251 MW;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M20035, AAA42241.1; -.
EMBL, M86564, AAA40758.1; -.
EMBL, M33024, AAA41931.1; -.
EMBL, X55326, CAA39028.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 EMDPPNPEEVKTPEEGE 111
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SEQUENCE
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us-09-782-745-27.closed.rsp

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"The primary sequence of the PFK-1 inactivating zinc-binding protein as deduced from cDNA sequencing. Identity of the zinc-binding protein with rat parathymosin "; FEBS Lett. 253:63-66(1989).
                                                                                             SEQUENCE FROM N.A.
STRAIN-FIGURER; TISSUE-Liver;
STRAIN-FIGURER; TISSUE-Liver;
MEDINE-92183876; PubMed-1544455;
Trompeter H.-I., Soeling H.-D.;
"Cloning and characterisation of a gene encoding the 11.5 kDa zinc-binding protein (parathymosin-alpha).";
FEBS Lett. 298:245-248(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 155:539-545(1988).
-!- FUNCTION: Parathymosin may mediate immune function by blocking the effect of prothymosin alpha which confers resistance to certain opportunistic infections.
                                                                                                                                                                                                                                                                                      MEDLINE-88239673; pubMed=3377505;
Frangou-Lazaridis M., Clinton M., Goodall G.J., Horecker B.L.;
"Prothymosin alpha and parathymosin: amino acid sequences deduced
from the cloned rat spleen cDNAs.";
Arch. Biochem. Biophys. 263:305-310(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISION TO 1-4.
MEDLINE=88339930; PubMed=3421960;
Panneerselvam C., Clinton M., Wellner D., Horecker B.L.;
"Bovine parathymosin: amino acid sequence and comparison with rat
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY SEQUENCE.
MEDIANE-86149281; PubMed-3456585;
MCDIANE-86149281; PubMed-3456585;
Chanlyama T., Pan L.-X., Haritos A.A., Wideman J.W., Pan Y.-C.E.,
Chang M., Rogers I., Horecker B.L.;
"The primary structure of rat parathymosin.";
Proc. Natl. Acad. Sci. U.S.A. 83:1242-1245(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 1-30.
MEDLINE-85140226; Pubmed-3856246;
Haritos A.A., Salvin S.B., Blacher R., Stein S., Horecker B.L.;
"Parathymosin alpha: a peptide from rat tissues with structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASP/GLU-RICH (ACIDIC).
D32BE03032BDB5D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nomology to prothymosin alpha.";
Proc. Natl. Acad. Sci. U.S.A. 82:1050-1053(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immune response; Acetylation; Zinc.
INIT MET 0 0
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EMBL; X64053; CAA45411.1; ALT_SEQ.
EMBL; X16481; CAA34501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11428 MW;
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                                                                                                                                                                                                                                                    SEQUENCE OF 22-101 FROM N.A.
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PIR; A05095; A05095
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PIR; B32265; B32265.
PIR; S05212; S05212.
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SEQUENCE
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MOD_RES
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                  38 EEEENGABEEEEEETAEDGEDD----DEGDEEDEEEE------EEDEGPVRKRTAEEE 85
EEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGP----DGQEM 96
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TISSUE-Small intestine;
Winterce A.K., Fredholm M., Davies W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERWATOGENESIS AND/OR
TESTIS DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostom1;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Procyclic form specific polypeptide A-alpha precursor (Procyclin alpha) (PARP A-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PQTGCECEDGP--DGQEM------DPPNPEEVKTPEEG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Made-enhanced antigen-1 (Mea-1) (Fragment).
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MEDLINE-89261740; Pubmed-2725502;
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                                                                                                                                                                                    97 DPPNPEEVKTPEEG 110
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DEADPKROKT-ENG 98
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P18764;
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Q95313;
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PARA_TRYBB
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4

Gaps

17;

Length 101; Indels

9.5%; Score 61.5; DB 1; 25.7%; Pred. No. 1.9e+02; iive 15; Mismatches 23;

Conservative

Best Local Similarity Matches 19; Conserv

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGAS-----AGQGPKPE---AHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGE 111
                                                              MEDLINE-90258895; PubMed-2342468; MEDLINE-90258895; PubMed-2342468; Clayton C.E., Fueri J.P., Itzhaki J.E., Bellofatto V., Sherman D.R., Wisdom G.S., Vijayasarathy S., Mowatt M.R.; "Transcription of the procyclic acidic repetitive protein genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Aggrecan core protein (Cartilage-specific proteoglycan core protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-
                                                                                                                                                                                                      G-P-E-E-T.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
               regulated brucei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61; DB 1; Length 114; Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFF2690DAAAE445E CRC64;
Mowatt M.R., Wisdom G.S., Clayton C.E.;
"Variation of tandem repeats in the developmentally
procyclic acidic repetitive proteins of Trypanosoma
Mol. Cell. Biol. 9:1332-1335(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                           DIFFERENTIATION IN THE INSECT VECTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPI-ANCHOR
                                                                                                                                     Trypanosoma brucei.";
Mol. Cell. Biol. 10:3036-3047(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Antigen; Repeat; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11611 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M25787; AAA53283.1; -. EMBL; M33129; AAA30224.1; -. EMBL; X52584; CAA36814.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27
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PIR; S21539; S21539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 KQSQ 115
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                                                                                                                                                                                             STRAIN=427;
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PGCA_PIG
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                                                                                                                                                                                                                                                               PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT ALSO KERATAN SULFATE CHAINS, N-LINKED AND O-LINKED OLIGOSACCHARIDES (BY SIMILARITY). SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                   FIX BIO1. 14:323-328(1994).
FUNCTION: THIS PROTEGLICAR
BUNCTION: THIS PROTEGLICAR
BUNCTION: THIS PROTEGLICAR
BATRIX OF CARPILLAGENOUS TISSUES. A MAJOR FUNCTION OF THIS PROTEIN
IS TO RESIST COMPRESSION IN CARTILLAGE. IT BINDS AVIDLY TO
HYALURONIC ACID VIA AN AMINO-TERMINAL GLOBULAR RESGION. MAY PLAY A
SUBCELLUONY ROLE IN THE MATRIX ASSEMBLY OF THE CARTILAGE.
SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clinton M., Frangou-Lazaridis M., Panneerselvam C., Horecker B.L.; "The sequence of human parathymosin deduced from a cloned human kidney cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                 TISSUE=Cartilage;
MEDLINE=9512652; bubMed=7827755;
Barry F.P., Neame P.J., Sasse J., Pearson D.;
"Length variation in the Keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99DC5641CBCD44A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 60.5; DB 1;
llarity 27.3%; Pred. No. 1.8e+02;
Conservative 9; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Cartilage; Proteoglycan; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR000538; Link.
Interpro; IPR001304; lectin_c.
PROSITE; PS01241; LINK; PARTIAL.
PROSITE; PS00615; C_TYPE_LECTIN_1; PARTIAL.
PROSITE; PS50041; C_TYPE_LECTIN_2; PARTIAL.
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MEDLINE=89149806; PubMed=2537638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S74664; AAC60528.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8576 MW;
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83
83 AA;
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                                                                                                                                                                                                                                                  SIMILARITY)
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                                                                                                        aggrecan.";
Matrix Biol
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SEQUENCE
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Matches 2
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PIR; A01520;
PIR; S06426;
                                                                     Acetylation;
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P05768;
                                                                                                                                                                           MOD_RES
MOD_RES
SEQUENCE
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                                                                                                            MOD_RES
DOMAIN
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RL12_HALHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 EEGEPATORODPAAAQEGEDEGASAGGGPKPEAHSQEQGHPQTGCECEDGP----DGQEM 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                         I- FUNCTION: Parathymosin may mediate immune function by blocking
the effect of prothymosin alpha which confers resistance to
certain opportunistic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93050183; PubMed-1426245;
Barcia M.G., Castro J.M., Jullien C.D., Gonzalez C.G., Freire M.;
"Prochymosin alpha is phosphorylated by casein kinase-2.";
FEBS Lett. 312:152-156(1992).
-I- FUNCTION: Prochymosin alpha may mediate immune function by conferring resistance to certain opportunistic infections.
-I- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Low T.L.K., Goldstein A.L.;
The chemistry and blology of thymosin. II. Amino acid sequence
analysis of thymosin alphal and polypeptide betal.";
J. Biol. Chem. 234:987-995(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88339364; PubMed-2901823;
Pannesralvam C., Wellner D., Horecker B.L.;
"The amino acid sequence of bovine thymus prothymosin alpha.";
Arch. Blochem. Biophys. 265:454-457(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLATION (BY SIMILARITY).
ASP/GLU-RICH (ACIDIC).
D42A6C04B25741C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
  Commun. 158:855-862(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%; Score 60.5; DB 1; Best Local Similarity 25.7%; Pred. No. 2.2e+02; Matches 19; Conservative 15; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Prothymosin alpha.
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MEDLINE-79109664; Pubmed-762108;
                                                                                                                                                                                                                                                                                                                                                                                                                                              11399 MW;
                                                                                                                                                                                                                                                                                                                                                           Immune response; Acetylation.
                                                                                                                                                                                                                                                                                          EMBL; M24398; AAA61185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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MIM; 168440; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              101 AA;
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P01252;
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Blochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                               38 ATPEEGEPATQRQDPAAAQEG--EDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein gene cluster of the halophilic archaebacterium Halobacterium
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MEDLINE-89305527; Pubmed-2743981;
Shimmin L.C., Dennis P.P.;
"Characterization of the Lil, Ll, Ll0 and Ll2 equivalent ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein operon
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                                                                                                                                                                                                                                                                                                                         Length 109;
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Structure, function and genetics of ribosomes, pp.326-361,
Springer-Verlag, New York (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                        PHOSPHORYLATION (BY CK2).
PHOSPHORYLATION (BY CK2).
PHOSPHORYLATION (BY CK2).
ECB151F0A9F99D24 CRC64;
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Eur. J. Biochem. 176:297-303(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of the ribosomal 'A'
                                                                                                                               ASP/GLU-RICH (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                               39.
                                                                                                                                                                                                                                                                                                                       9.2%; Score 59.5; DB 1; 23.0%; Pred. No. 2.7e+02; iive 13; Mismatches 39;
                                                                                  THYMOSIN ALPHA-1.
                            r protein; Phosphorylation.
28 πηνωρέτα
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NAY-2000 (Rel. 39, Last annotation update)
50S. ribosomal protein L12P ('A' type) (HL20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 AA.
                                                                                                        ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES-H.halobium; STRAIN-S9;
MEDLINE-88329082; Pubmed-2458258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-H.halobium; STRAIN-A9;
                                                                                                                                                                                                                                             11941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 8:1225-1235(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacterium halobium, a
Halobacterium cutirubrum.
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 MDPPNPEEVKTPEE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VD---TKKQKTDED 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2242, 2242;
TNBOA1.
S06426.
Nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wittmann-Liebold B.;
                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                            Yaguchi M., Matheson A.T., Visentin L.P., Zuker M.;

Yaguchi M., Matheson A.T., Visentin L.P., Zuker M.;

Yolo Osawa S., Ozeki H., Uchida H., Yura T. (eds.);

Genetics and evolution of RNA polymerase, trNA and ribosomes,

pp.585-599, University of Tokyo Press, Tokyo (1980).

-! FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS

INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION.

-! SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 EVEPATPEEGEPATORODPAAAQEGEDEGASAGGGPKPEAHSQEQGHPQTGCECEDGPDG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.2%; Score 59.5; DB 1; Length 114; Best Local Similarity 24.6%; Pred. No. 2.8e+02; Matches 16; Conservative 7; Mismatches 27; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 AA; 11562 MW; CBEB2E38BD4A644C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X06736; CAA29915.1; --
EMBL; X13008; CAA31432.1; --
EMBL; X13078; CAA33181.1; --
FIR; S01745; R5H23H.
FIR; S04121; R5H52H.
InterPro; IPR001813; 60s_ribosomal.
Ffam; PF00428; 60s_ribosomal;
Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: July 1, 2002, 06:39:48
Job time: 189 sec
[5]
SEQUENCE OF 1-76.
SPECIES-H.cutirubrum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 DDEEP 104
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-782-745-27 Title:

Perfect score:

646 1 MSWRGRSTYRPRPRRYVEPP......DPPNPEEVKTPEEGEKQSQC 116 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 segs, 172994929 residues Searched:

133496 Total number of hits satisfying chosen parameters:

length: 0 length: 116 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL\_19:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*

sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* sp\_mhc:\* sp\_organelle:\* sp\_phage:\*

sp\_unclassified:\* sp\_virus:\* sp\_vertebrate:\* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* sp\_rodent:\*

sp\_plant: \*

10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q9ueu5 homo sapien	Q96qt9 homo sapien	homo	stron			09qzk1 cavia porce	Q85063 cottontail	O66642 equine herp	015215 homo sapien	Q23793 chironomus	09n3b4 caenorhabdi	09kil8 streptomyce	09kyf6 streptomyce		
	ID	Q9UEU5	Q96GT9	Q96GU1	018562	Q9GYX8	P87914	Q9QZK1	085063	066642	015215	Q23793	Q9N3B4	Q9KIL8	Q9KYF6	Q9Y3S3	Q9H1E6
	ength DB	16 4	<b>4</b> 11	10	90 5	08 5	90 12	74 11	81 12	91 12	93 4	99 5	07 5	75 2	14 2	100 4	114 4
	~	<b>&gt;</b>	_	_	•	1	_										
dР	Query	98.6	35.5	16.6	13.1	12.8	12.2	11.8	11.6	11.5	11.1	11.1	11.1	11.0	11.0	10.9	10.9
	Score	637	229.5	107.5	84.5	82.5	79	97	75	74.5	72	71.5	71.5	7.1	7.1	70.5	70.5
	Result No.	1	2	e	4	ស	9	7	œ	თ	10	11	12	13	14	15	16

RESULT

Q9yepO aeropyrum pol8928 macaca radio23794 chironomus Q91164 homo sapien Q91468 streptomyce G9vug5 drosophila O80818 arabidopsis Q9gx4 canis famil Q15254 homo sapien Q9vps9 drosophila Q13902 homo sapien Q94v59 canis famil Q9ued2 homo sapien Q923p0 mus musculu Q923p0 mus musculu Q923p0 mus musculu Q9vps8 drosophila Q9vps8 drosophila Q9vps8 drosophila Q9dQ18 mus musculu Q9vps8 drosophila Q9dQ18 mus musculu Q95p0 mus musculu Q9vps8 drosophila Q9vps8 drosophila Q9dQ18 mus musculu Q15202 homo sapien Q9fhO0 arabidopsis	Q9yb29 aeropyrum p Q9df10 g111ichthys Q9buf2 xenopus lae
09YEPO 018928 09ULQ8 09ULQ8 09VUQ5 09VUQ5 09FX81 015254 015254 015254 015254 015254 019759 09FX91 091759 09TV59 09TV59 09TV59 09TV57	Q9YB29 Q9DFL0 Q98UF2
100 100 100 100 100 100 100 100 100 100	
101 108 108 108 108 108 108 108 108 108	116 53 106
0.000000000000000000000000000000000000	
000 0 0 000 000 000 000 000 000 000 00	
111 122 133 133 133 133 133 133 133 133	4 4 4 6 4 5

## ALIGNMENTS

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1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGED 60
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                               MEDLINE-99323388; PubMed=10397259;
MEDLINE-99323388; PubMed=10397259;
De Backer O., Arden K.C., Boretti M., Vantomme V., De Smet C., Czekay S., Viars C.S., De Plaen E., Brasseur F., Chomez P., Van den Eynde B., Boon T., Van der Bruggen P.;
"Characterization of the GAGE genee that are expressed in various human cancers and in normal testis."
Cancer Res. 59:3157-3165(1999).
EMBL; ARO55473; AAC33676.1; -.
SEQUENCE 116 AA; 12764 MW; DDZ652939E66F19A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                             Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.6%; Acore 637; DB 4; L. Best Local Similarity 99.1%; Pred. No. 5.1e-50; Matches 115; Conservative 0; Mismatches 1;
                                  116 AA
                                                               Created)
                                PRT;
                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                              PRELIMINARY;
                                               Q9UEU5;
                                                                                                           GAGE-8.
                             Q9UEUS
RESULT
Q9UEUS
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4

Gaps 69

27;

33;

Length 90; Indels

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Toledo R., Rodriguez-Medina J.R., Hillyer G.V.;
"Molecular cloning and characterization of a Fasciola hepatica gene-
mociding a proline-rich polypeptide related to tegumental antigens.";
Submitted (Jul. 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF286861; AAG00994.1;
InterPro: IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
NON_TER
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IGG AND IGE IMMUNOREACTIVE ANTIGEN RECOGNIZED BY SERA FROM PATIENTS
WITH STRONGYLOIDIASIE (FRAGMENT).
Strongyloides stercoralis.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoldea; Strongyloididae; Strongyloides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fasciola hepatica (Liver fluke).
Eukaryota, Metazoa, Platyhelminthes; Trematoda; Digenea;
Echinostomida; Echinostomata; Fascioloidea; Fasciola.
                                                                                                                                                                                                                                                                                                                           10 RPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGP
                                                                                                                                                                                                                                                                                                                                            24 GPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQT
                                                                                                                                                                             EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9C208DDE3F050055 CRC64;
                                                                                                                    SEQUENCE FROM N.A.
Ramachandran S., Thompson R.W., Gam A.A., Neva F.A.;
"A set of recombinant clones for immunodiagnosis of strongyloidiasis.";
                                                                                                                                                                                                                       90 AA; 9438 MW; D2373206920E68B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
TEGUMENTAL ANTIGEN-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                    70 KPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEG 110
                                                                                                                                                                                                                                                                                                                                                                                                    53 EGPAGPEEPEGPEG-----PEG----PAGPEEPRDDDDG 82
                                                                                                                                                                                                                                                                 13.1%; Score 84.5; DB 5; 24.8%; Pred. No. 1.1; tive 16; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82.5; DB
Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 GCECEDGPDGQEMDP-PNPEEVKTPEE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA; 11325 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%;
32.2%;
                                                                                                                                                                         Submifted (FEB-1997) to the EMBL; U90352; AAB65140.1; -. NON_TER 1 1
                                                                                                                                                                                                                                                                                  Best_Local Similarity 24.8
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6192;
                                                                                        NCBI_TaxID=6248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 28;
                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                     Query Match
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P87914;
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                                                                                                                                                                                                                                                                                                                                                                       1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPA--TPEEGEPATORODPAAAQEG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                 E-DEGASAGQPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                               4; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.6%; Score 107.5; DB 4; Length 110; 32.7%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 SAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQ 113
                                                                                                                                                                                                                                                                                              ch 35.5%; Score 229.5; DB 4; Length 1 Similarity 45.8%; Pred. No. 1.5e-13; 54; Conservative 15; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                    Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC009232; AAH09232.1; -.
SEQUENCE 111 AA; 12354 MW; 38C93332C5BA0E14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ database.
EMBL; BC009230; AAH09230.1; -.
SEQUENCE 110 AA; 11777 MW; 6D6AF4563135BB6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:16481).
                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
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                   111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=PLACENTA, AND CHORIOCARCINOMA;
                                               Created)
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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05,
                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, SIMILAR TO G ANTIGEN 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Conservative
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                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Matches 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=MELANOMA;
                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                          Strausberg R.;
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01.JAN-1998
01.JAN-1998
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                  096GT9
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Matches
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Q96GU1
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Gaps 83

19;

Indels

34;

5; Length 108;

------PKP-----GPEP 53

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81

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STRAIN-WASHINGTON B;
MEDLINE-85166175; PubMed-2984661;
Giri I., Danos O., Yaniv M.;
"Genomic structure of the cottontail rabbit (Shope) papillomavirus.";
Proc. Natl. Acad. Sci. U.S.A. 82:1580-1584(1985).
EMBL; U09497; AAB60544.1;
                                                                                                                                                                                           Wu X., Brandsma J.; "Papilloma Formation by Cottontail Rabbit Papillomavirus (CRPV) Requires El and E2 Regulatory Genes in Addition to the E6 and E7
                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PAPILLOMAVIRUS SYLVILAGI WASHINGTON B (E2) AND (E4) GENES
                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                            Cottontail rabbit papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.6%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                81 AA; 9173 MW;
                PRELIMINARY;
                                                                                                                                                                                                                                 Transforming Genes."; J. Virol. 0:0-0(1994)
                                                                                                                                                                                   STRAIN-WASHINGTON B;
                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                 Papillomavirus.
NCBI_TaxID=10623;
                                                                                     (FRAGMENT).
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SEQUENCE
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  Q85063
ID Q85063
AC Q85063;
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Q66642
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                                                                                                                                                                                                                                                                                                                             -----DSG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSTYRPRRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RKTGGEQPK--VEAPABIKPTEP---TGPTEPPQPE--QPPQPEQPPQPEQPPQPE--- 52
                                                                                                                                          Carter K.L., Rolzman B.;
"Alternatively spliced mRNAs predicted to yield frame-shift genes a stable intron 1 RNAs of the herpes simplex virus 1 regulatory gene alpha o accumulate in the cytoplasm of infected cells.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1996).
EMBL; U70040; AAB37297.1; -. SEQUENCE 90 AA; 9210 MW; 9B0562ECF6D55C8C CRC64;
                                                                                                                                                                                                                                                                                                    5 GRSTYRP--RPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76; DB 11; Length 74;
Pred. No. 5.3;
7; Mismatches 34; Indels
                                                                                                                                                                                                                                                      Score 79; DB 12; Length 90; Pred. No. 3.5;
                                                                                                                                                                                                                                                                              25; Indels
                                                                        RNA stage; Herpesviridae;
 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  63 ASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPE 102
                                                                                                                                                                                                                                                                                                                   | || || || ||:| |||| : | |
6 GASTRRPEGRPQR-EEPPAIFGGRR------GTP-
                                                                                                                                                                                                                                                                                                                                                                        ASGGREKREEEGSGSKGRTQTTFGC----RPLSPPSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                   74 AA
                                                                                                                                                                                                                                                                              8; Mismatches
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                                                                     Viruses; dsDNA viruses, no RNA sta
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                      12.2%;
29.0%;
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11.8%;
Best Local Similarity 32.9%;
Matches 26; Conservative
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03,
19,
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                                                                                                                                                                                                                                                                              Conservative
 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. )
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                           human herpesvirus 1.
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 29; Conserva
                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10141;
                                                                                              NCBI_TaxID=10298;
01-MAY-1997
01-MAY-1997
01-DEC-2001
                                                                                                                                 STRAIN-F;
                                                ALPHA 0.
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Length 81;

4E80200A0004DF5C CRC64;

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 91;
                                                                                67 QGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQ 115
                                         25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Telford E.A.R.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20824; AAC13826.1; -
SEQUENCE 91 AA; 10311 MW; 1784D979FAA61F40 CPC64.
                                                                                                         |||||| ::| :: | :: | OGPKPRVHWADEGGGHQG--CNEGRQSNENRPPRTKRILLPGTSDRLLQ
                                                                                                                                                                                                                                                                                                                                            Equine herpesvirus type 2 (strain 86/87) (EHV-2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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Score 75; DB 12;
Pred. No. 7.1;
7; Mismatches 25;
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Pred. No. 8.9;
9; Mismatches
                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                               Created)
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01-NOV-1996 (TrEMBLrel. 01, Las
01-OCT-2001 (TrEMBLrel. 18, Las
MYRISTYLATED TEGUMENT PROTEIN.
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30.8%;
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Best Local Similarity 30.00,
                                                                                                                                                                                                                       PRELIMINARY;
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SEQUENCE FROM N.A.
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Query Match
Best Local Similarity
Matches 22; Conserv
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Q9KIL8;
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Q9N3B4
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ID 09
AC 09
DT 01
DT 01
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                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HIGH MOBILITY GROUP PROTEIN I/Y.
Chironomus tentans (Midge).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                       Score 72; DB 4; Length 93; Pred. No. 15;
                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                           67 QGPKPEAHSQEQGHP-----QTGCECED--GPDGQEMDPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematocera;
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Chironomoidea; Chironomidae; Chironominae; Chironomus
                                                                                                                                                                                                                                                              04AD5F0797E31867 CRC64;
                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SALIVARY PROLINE-RICH PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 81:5561-5565(1984)
EMBL; K02576; AAA36503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        99 AA.
                                                                                     93 AA
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                                                                                      PRT;
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                                                                                                                                                                                                                                                                                        11.1%; 25.3%;
                                                                                                                                                                                                                                                              93 AA; 9170 MW;
                                          83
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Matches 19; Conservative
                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                            100 -NPEEVKTPEEGEKO 113
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                         96 MDPPNPEEVKTPEEGEKQ
                                          66 GREPOPEVKTTPYPKRKK
                                                                                                                                                                                                                                                                                                                                                                        63 GNPQQPQAPPAGQPQ 77
                                                                                                                                                                                 SEQUENCE FROM N.A.
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NCBI_TaxID=7153;
                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                             proteins."
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SEQUENCE
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                           Gaps
                                                                               10 RPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQ-G 68
                                                                                                      6 NSDSQKSLPSPGHPSTGRPDLDLITDPLEEQRLE-----PORDSHRSDTRGHPSTG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 SDEVEPATPEEGEPATQR-----QDPAAAQEGEDEGASAGQGPKPEAH-SQEQGHPQTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                           3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 107;
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                                         43; Indels
    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2;

WD01am C., Zidanic M.;

"The sequence of C. elegans cosmid Y54G2A.";

submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Last annotation update)
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    DB 5;
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                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71.5;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                      107
    Score 71.5;
Pred. No. 18
                                                                                                                                                                                       69 PKPEAHSQEQGHPQTGCECEDGPDGQEMD 97
                                                                                                                                                                                                                                                                                                                                            Created)
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MEDLINE-99069613; PubMed-9851916;
11.1%; Sco
llarity 24.7%; Pre
Conservative 21;
                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, CX 01-0CT-2000 (TrEMBLrel. 15, La 01-DEC-2001 (TREMBLrel. 19, La HYPOTHETICAL 11.9 KDA PROTEIN.
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25.8%;
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Best Local Similarity 25.8%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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"Direct Submission.";
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STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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SEQUENCE
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AR23040975; CAC01372.1;

EMBL; AL390975; CAC01372.1;

SEQUENCE 75 AA; 8263 MW; 392569EF4D29B941 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           IGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Attinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. NCBL_TaxID=1902;
                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                  [1]
SEQUENCE FROM N.A.
STRAIN-A3(2), AND M145;
Kormanec J., Sevcikova B., Homerova D.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
Oliver K., Harris D.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                  STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                    Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE SECRETED PROTEIN (FRAGMENT).
SCC61A.37C.
                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                             11.0%; Score 71; DB 2; 27.8%; Pred. No. 15; Live 10; Mismatches 3
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(HYPOTHETICAL 8.3 KDA PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE-97000351; Pubmed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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          F58A OR SCP8.34C.
Streptomyces coelicolor.
                                                                                                                                                          Harris D.;
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Best Local Similarity
Matches 25; Conserv.
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Bentley S.D.,
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                                                                                                                                                                                                                                                                                                                   32 SDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGP 91
                                                                                                                                                                                                                                                                                                                                              Kinashi M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map
the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL, AL356595; CAB92282.1; -.
SEQUENCE 114 AA; 11673 MW; EC396FC15B4B9991 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Walter A.O., Schwaeble W.J., Thres T., Radecke K., Real F.X., Dippold W.; "Cloning and characterisation of a novel human mucin gene with 53-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 23;
8; Mismatches 39; Indels
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AJU06205; CABJ492.1; -.
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Last annotation update)
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11009 MW;
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                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.8%;
Matches 25; Conservative
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MUC-B1.
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Job time: 195 sec
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July 1, 2002, 06:33:09; Search time 23.51 Seconds (without alignments) 548.046 Million cell updates/sec
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1 MSWRGRSTYRPRPRRYVEPP......DPPNPEEVKTPEEGEKQSQC 116
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 116
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... /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	GAGE2 polypeptide.	GAGE-Z CUMOUI LEJE Human secreted pro	Human polypeptide	Novel human diagno	Human polypeptide	Human protein SEQ	Human cell cycle a	Novel human diagno	Human NOV4 protein	PAGE-4 polypeptide
CHANGING	ΩI	AAY83159	AAG02123	AAM39588	ABG05297	AAM41374	AAM78785	AAB60500	ABG05299	AAE08583	AAY83158
	DB	21	21	22	22	22	22	22	22	22	21
	% Query Match Length DB	116	110	111	112	106	111	111	09	115	102
	% Query Match	100.0	61.9	42.0	41.6	38.6	35.5	35.5	24.1	21.8	18.6
	Score	646	400	271.5	268.5	249.5	229.5	229.5	155.5	141	120
	Result No.	, n	<b>7</b> 1 (C)	4	Ŋ	9	7	80	σ	10	11

AAY5298         Human secreted pro           AAK83167         Human NOV2 protein           AAK83167         Human NOV2 protein           AAX12447         Human NOV3 protein           AAX12447         Human NOV3 protein           AAX29429         AAX29429           AAX29429         CAGE tumour rejection a           AAX29429         CAGE tumour rejection a           AAX29429         CAGE tumour rejection a           AAX802997         Protein #2602 enco           AAM56001         Human bone marrow           AAM68370         Peptide #261 enco           AAM32534         Peptide #259 enco           AAM32534         Silver halide emul           AAW3253         Collagen-like poly           AAW3253         Collagen-like poly           AAW12340         Collagen-like poly           AAW1232         Collagen-like poly           AAW41712         AAW41712           AAW41712<	AA.  testis histocom response  response  in g in ing anti cell sa
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1111 89 33 33 33 35 35 35 35 35 35 35 35 35 35	rote entr repr ncer te; te; TH & US2(
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	59 standard; Pro 59; -2000 (first en polypeptide. ; placenta; canc xxic T lymphocyte conjugate. :apiens. 112706-Al (-2000. ) US DEPT HEALTH ) US DEPT HEALTH ) US DEPT HEALTH ) US DEPT HEALTH con DEPT HEALTH ) US DEPT HEALTH  DEPT HEALTH  DEPT HEALTH  US
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WPI; 2000-500381/45.
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                                                        The productive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms.

An isolated PAGE-4 peptide which induces a cytotoxic T in tesponse when bound to a major histocompatibility complex. Immunogenic compositions to raise a cytotoxic T lymphocyte response immunogenic compositions to raise a cytotoxic T lymphocyte response immunogenic compositions to raise a cytotoxic T lymphocyte response against cells expressing PAGE-4 including cancer cells of the PAGE-4 peptide fragments can also be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in cells cancering the presence of PAGE-4 and PAGE-4 coding sequences in cell cancerous reproduction can be indicative of the spread of cancerous reproduction can be indicative of the spread of cancerous reproduction can be indicative of the spread of antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems. The PAGE family of the profession of the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                     male and female
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                                                 is a gene preferentially expressed in normal
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100.0%; Pred. No. 8.3e-53;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Thr encoded by CCT"
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               Disclosure; Figure la; 63pp; English.
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Best Local Similarity 100.
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 116 AA;
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The present sequence represents a GAGE-2 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPS have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGED 60
                                                                                                                                                            Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 mswrgrstyrprrryveppemigpmrpeqfsdevepatpeegepatgrqdpaaaqeged 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 638; DB 19;
Pred. No. 4.6e-52;
0; Mismatches 1;
Van Den Eynde B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein, SEQ ID NO: 6204.
                                                                                                                                                                                                                                                                                               Example 13; Fig 5; 60pp; English.
Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.8%;
Best Local Similarity 99.1%;
Matches 115; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG02123 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-2000; 2000EP-0200610.
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                                                          1998-076905/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 AA;
Boon-Falleur T,
                                                                                                 N-PSDB; AAV18717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033401-A2
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Drmanac RT, Liu C,
                                     Zhao OA,
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                Tang YT,
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                                                                                     The present sequence is a polypeptide encoded by one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; hamostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                     Length 76;
                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                  Score 400; DB 21;
Pred. No. 4e-30;
0; Mismatches 2;
                                                                  Claim 13; SEQ ID 6204; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM39588 standard; Protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 2733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                                                                                  Query Match 61.9%;
Best Local Similarity 97.3%;
Matches 73; Conservative (
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        82 QTGCECEDGPDGQEM 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
 N-PSDB; AAC02129.
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14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM39588;
                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification.
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        Wang
                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 GEDEGASAGOGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQ 115
     Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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     Qian XB,
Yang Y,
, Ma Y, (Xue AJ,
                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 2733; 10078pp; English.
                                                          Goodrich R, Drmanac RT;
  Asundi V, Chen R,
Wehrman T, Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG05297 standard; Protein; 112 AA
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                WPI; 2001-442253/47.
Liu C, A
Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                          N-PSDB; AAI58744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.N.S disorders.
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23-AUG-2000;
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21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                              Zhao OA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                  Wang
δ
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                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of ridentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating replypeptide and polynucleotide sequences have applications in disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in claspnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                               and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaimer's; Parkinson's disease; hademostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemctactic; chemckinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPA--TPEEGEPATQRODPAAAQE- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.6%; Score 268.5; DB 22; 49.2%; Pred. No. 1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                Claim 20; SEQ ID No 35656; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM41374 standard; Protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 6305.
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Best Local Similarity 49.28
Matches 58; Conservative
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           WPI; 2001-639362/73.
N-PSDB; AAS69484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1
                                                                                                      biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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AAM41374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's parkinson's disease, Huntington's disease, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotoctic/chemokinetic activity, nemeterclic/chemokinetic activity, nemeterclic/chemokinetic activity, nemeterclic/chemokinetic activity, amenostatic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                         Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSWRGRSTYRPRRRYVEPPEMIGPMRPEQFSDEVEPA--TPEEGEPATQRQDPAAAQE-
                                                                                                                                                                                                                                                                                          Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.6%; Score 249.5; DB 22; Length 106; 50.5%; Pred. No. 5.7e-16; 1ve 10; Mismatches 34; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang Y,
                                                                                                                                                                                                                                                         Liu C, Asundi V, Chen R, Ma Y, ang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 6305; 10078pp; English.
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09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SFP-2000; 2000US-0662191.
19-OCT-2000; 2000US-069336.
29-NOV-2000; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442253/47.
                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 106 AA;
                                                                                                                                                                                                                                                               Liu C,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAI60530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification.
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Sednence
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ABG05299
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                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine. Cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heamatopoiesis regulating activity issue growth factor activity, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or inflammation.
                                                                                                                                                                                      Υ;
                                                                                                                                                                                                                                                                                                                                                                                                                            Vote: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing vere missing at the time of publication.
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                                                                                                                                                                                       Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell cycle and proliferation protein CCYPR-48, SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPA--TPEEGEPATQRQDPAAAQEG
                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                      Cao Y,
                                                                                                                                                                                                ZW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 111;
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Wang ?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Indels
                                                                                                                                                                                    Liu C, Drmanac RT, Asundi V, Zhou P, Xu (Wang D, Wang J, Zhang J, Ren F, Chen R, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonist; gene therapy; detection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.5%; Score 229.5; DB 2 45.8%; Pred. No. 4.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                                                                                                                                          Claim 20; Page 3714-3715; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60500 standard; Protein; 111 AA
                                                                              2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
                                                                                                                       2000US-0663561.
2000US-0693325.
2000US-0728422.
                                                 05-FEB-2001; 2001WO-US04098
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N-PSDB; AAK51918.
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                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA;
         WO200157190-A2.
                                                                                                   19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                          20-JUN-2000;
                                                                      03-FEB-2000;
                                                                                 27 - APR - 2000;
                                                                                                                                             30-NOV-2000;
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                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                    Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB60500;
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Best Local 9
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AAB60500
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proliferation proteins (CCYPR), which are encoded by AAF59543.

CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with core confounds or so that the confound of functional CCYPR. Monoclonal or plyclonal antibodies to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioimmunoasays to detect CCYPR. CCYPR itself may be used to detect compounds e.g., antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR. CCYPR itself may be used to dener the activity of CCYPR. CCYPR identify compounds that modulate the activity of CCYPR. CCYPR incledides can be used to generate transgenic animal models of human disease, and can be used to generate transgenic animal models of human classase, which can be disequosed, treatment or prevention of a disorder associated with CCYPR. CTYPR. CTYPR proteins, nucleic acids, agonists or antagonists include immune, developmental and cell signalling disorders, and call proliferative developmental and cell signalling disorders, asthma, cancer, allergies, allebers, mellitus, disorders of the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cell cycle and proliferation proteins and polynucleotides are
transgenic animal disease model; immune disorder;
developmental disorder; cell signalling disorder;
cell proliferative disorder; cancer; tumnour; anaemia; epilepsy;
arteriosclerosis; aschma; allergy; diabetes mellitus;
menstrual cycle disorder; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bandman O;
C, Shah P;
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Baughn MR, Patterson
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45.8%; Pred. No. 4.3
:ive 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT,
Lu DAM,
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99US-0153129.
99US-0164647.
                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000; 2000WO-US19948.
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Matches 54; Conservative
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Yang J,
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                                                                                                                                                                                                                                                                      WO200107471-A2
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08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                         01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caused by
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AAE08583 standard; Protein; 115 AA.
                                                               AAE08583;
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                          AAE08583
                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The choice tides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
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7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 35658; 103pp; English.
                                                                          Novel human diagnostic protein #5290.
ABG05299 standard; Protein; 60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.1%;
50.0%;
                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
N-PSDB; AAS69486.
                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
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                                                                                                                                                                 WO200175067-A2.
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                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           biodiversity
                                                                                                                                                                                           11-0CT-2001.
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The present sequence is a human NOV4 protein. The NOVX protein has homology with one of G-antigen (GAGE)-like protein, interferon G-protein coupled receptor (GPCR), hepatocyte nuclear factor or mast cell protease. The NOVX is useful for treating or preventing a pathology associated with NOVX. It is also useful for determining the presence or amount of NOVX DNA in a sample, for identifying a potential therapeutic agent and in gene therapy. It is also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX. It is also useful for the diagnosis and treatment of proliferative disorders, e.g., cancer, immune disorders, hepatic disorders, e.g., cirrhosis, viral infections, e.g., hepatitis, neuroolfactory disease, infertility, autoimmune diseases, arthritis, multiple sclerosis, allergies and wound healing.
                                                                                                                                                           G-protein coupled receptor; GPCR; hepatocyte nuclear factor; mast cell protease; gene therapy; proliferative disorder; cancer; immune disorder; cancer; hepatic disorder; cirrhosis; viral infection; hepatitis; neuroolfactory system-related disorder; neurological disorder; Parkinson's disease; infertility; autoimmune disease; arthritis; multiple sclerosis; allergy; wound healing; cytostatic; nootropic; immunosuppressive; neuroprotective; vulnerary; hepatotropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer, infertility, autoimmune diseases, arthritis, multiple sclerosis, allergies, wound healing and hepatic disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated novel polypeptides useful for diagnosis of and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Tchernev VT, Padigaru M, Taupier RJ,
Guo X, Spaderna SK, Boldog FL;
                                                                                                                                Human; NOVX; G-antigen; GAGE-like protein; interferon;
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2000US-0182733.
2000US-0183896.
2000US-0184275.
2000US-0184482.
2000US-0184497.
2000US-0184497.
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2000US-0236060.
2001US-0259414.
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14-FEB-2001; 2001US-0783429
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514775/56.
N-PSDB; AAD14983.
                                                                   Human NOV4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200161009-A2.
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13-APR-2000;
10-AUG-2000;
27-SEP-2000;
27-SEP-2000;
02-JAN-2001;
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23-FEB-2000;
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23-FEB-2000;
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01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lymphocyte response when bound to a major histocompatibility complex (MHC) class I molecule or the isolated PAGE-4 protein can be used in immunogenic compositions to raise a cytotoxic T lymphocyte response against cells expressing PAGE-4 including cancer cells of the prostate, uterus and testis. The nucleic acids encoding PAGE-4 or PAGE-4 peptide fragments can also be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are not related to reproduction can be indicative of the spread of
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancerous reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reproductive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms. An isolated PAGE-4 peptide which induces a cytotoxic T
                                                                                        Indels 10;
                                                                                                                                                1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPA--TPEEGEPATQRQDP 52
                                                       Length 115;
                                                   Score 141; DB 22;
Pred. No. 7.6e-06;
9; Mismatches 7;
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                                                                                                                                                                                                                                                         AAY83158 standard; Protein; 102 AA
                                                 Query Match 21.8%;
Best Local Similarity 51.9%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US20046.
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N-PSDB; AAZ93524.
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115 AA;
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   Sednence
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                                        Gaps
                                                                     1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRODPAAAQEGED 60
                                                                                                 1 msarvrsrsrgrgdgg-eapdvva-----fvapgesggeepptdngdiepgg--er 48
                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; nutritional; cytokine; cell proliferation;
                                                                                                                                                                                                                                                                                                                                 Human secreted protein clone bn365_53 protein sequence SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                             differentiation; immune stimulating; vaccine; suppression; haematopolesis regulation; tissue growth; activin; inhibin; enemotatic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; atti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy.
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Steininger RJ, Bowman MR;
                                        12;
                                                                                                                                 61 EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQ 113
                                                                                                                                                   Length 102;
                                          Indels
10; Mismatches
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Treacy M, Agostino MJ,
mith E, Widom A;
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                                                                                                                                                                                                                                          AAY52998 standard; Protein; 102
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98US-0095880.
98US-0096068.
99US-0096068.
         18.6%;
34.5%;
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                                                                                                                                                                                                                                                                                                      (first entry)
                                          39; Conservative
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                           Local Similarity
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22-JUL-1998)
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10-AUG-1998
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06-MAY-1999
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Merberg D,
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           Query Match
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                                           Matches
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activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. AAZ33316 to AAZ33373 encode human secreted proteins, and AAY52998 to AAX53060 represent human secreted proteins, given in the
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reproductive tissues e.g. prostate. testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms.

An isolated PAGE-4 peptide which induces a cytotoxic T lymphocyte response when bound to a major histocompatibility complex (MHC) class I molecule or the isolated PAGE-4 protein can be used in immunogenic compositions to raise a cytotoxic T lymphocyte response against cells expressing PAGE-4 including cancer cells of the profitate, uterus and testis. The nucleic acids encoding PAGE-4 pottide fragments can also be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in
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                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                   EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQ 113
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                                                                                                                                                                                   Length 102;
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-hag 52; Indels
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                                                                                                                                                                                 DB
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                                                                                                                                                                               Score 120;
Pred. No. 0
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                                                                                                                                                                             18.6%;
34.5%;
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                                                                                                                                                                                            Best_Local Similarity 34.59
Matches 39; Conservative
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                                                                                           present invention.
                                                                                                                            102 AA;
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                                                                                                                            Sequence
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detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are not related to reproduction can be indicative of the spread of cancerous reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems. This sequence is of the PAGEI polypeptide which shares sequence similarity with
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                    1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRODPAAAQEGED 60
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                                                                                                                                                                                                         DB 21; Length 87;
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FL;
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Majumder K, Guo X, Spaderna SK, Boldog
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32.7%;
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2000US-0182724.
2000US-0182733.
2000US-0183896.
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2000US-0184744.
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2000US-0236060.
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2001US-0783429
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Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOV2 protein.
                                                                                                                                                          87 AA;
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22-FEB-2000;
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24-FEB-2000;
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The present sequence is a human NOV2 protein. The NOVX protein has homology with one of G-antigen (GAGE)-like protein, interferon, cell protean coupled receptor (GPCR), hepatocyte nuclear factor or mast cell protease. The NOVX is useful for treating or preventing a pathology associated with NOVX. It is also useful for determining the presence or amount of NOVX ban in a sample, for identifying a potential therapeutic agent and in gene therapy. It is also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX. It is also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX. It is also useful for the diagnosis and treatment of proliferative disorders, e.g., cancer, immune disorders, hepatic disorders, e.g., system-related disorders, meurological disorders, e.g., parkinson's system-related acceptor, meurological disorders, e.g., Parkinson's allergies and wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRODPAAAQEGEDEGA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated novel polypeptides useful for diagnosis of and treating cancer, infertility, autoimmune diseases, arthritis, multiple sclerosis, allergies, wound healing and hepatic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.0%; Score 109.5; DB 22; Length 111; 32.7%; Pred. No. 0.0063; Live 17; Mismatches 50; Indels 7;
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                                                                                                                                     Claim 1; Page 9; 140pp; English.
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PAGE-4 is a gene preferentially expressed in normal male and female reproductive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms.

An isolated PAGE-4 peptide which induces a cytotoxic T lymphocyte response when bound to a major histocompatibility complex immorpants compositions to raise a cytotoxid T lymphocyte response when bound to a major histocompatibility complex immunogenic compositions to raise a cytotoxid T lymphocyte response against cells expressing PAGE-4 including cancer cells of the prostate, uterus and testis. The nucleic acids encoding PAGE-4 or PAGE-4 peptide fragments can also be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in tissues which are not related to reproduction can be indicative of the spread of cancerous reproduction can be indicative of the spread of antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems. This sequence is coff the PAGE3 polypeptide which shares sequence similarity with
lymphocyte response and for raising antibodies which can be used to detect the presence of PAGE-4 in cell samples or body tissues
                                                                                      63pp; English
                                                                                Disclosure; Figure 1b;
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45 PATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEV 104 ï 16.8%; Score 108.5; DB 21; Length 79; 43.5%; Pred. No. 0.0054; Live 5; Mismatches 33; Indels 1 Best Local Similarity 43.5 Matches .30; Conservative Query Match ò

79 AA;

Sequence

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Gaps

KIPEEGEKQ 113 105 ò

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kipeagegg 76 89 qq

Search completed: July 1, 2002, 06:36:35 Job time: 206 sec

Isolated PAGE-4 protein and peptide used for inducing a cytotoxic  ${\tt T}$ 

WPI; 2000-237869/20.

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I55851 Sequence 14 BC018052 Homo sapi AX285022 Sequence U19143 Human GAGE-

Sequence 16

AF055473 Homo sapi AR028490 Sequence

AR028492 Sequence 155855 Sequence 18 AR028491 Sequence 18 AR028491 Sequence 115584 Sequence 175884 U19147 Human GAGE-U19147 Human GAGE-AF055874 Homo sapi AR028498 Sequence 15 U19144 Human GAGE-AR028489 Sequence 15 U19144 Human GAGE-AR028482 Sequence 15 U19144 Human GAGE-AR028482 Sequence 15 U19142 Human GAGE-

157317 Sequence 1 AX284692 Sequence AX284692 Sequence BC004861 Homo Sapi BC009232 Homo Sapi

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AJ318881 PAJ318880 P

Human DNA Human DNA Sequence Homo sapi

Z68274 Human DNA

AX078298 S BC009230 F

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Homo sap

AF235098

Sequence

OM nucleic

Run on:

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1 (bases 1 to 538)
van der Bruggen,P., van den Eynde,B., DeBacker,O. and
Boon-Falleur,T.
Isolated peptides derived from the gage tumor rejectio
precursor and uses thereof
Patent: US 5858689-A 14 12-JAN-1999;
Location/Qualifiers
1. 538
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Sequence 14 from patent US 5858689.
AR028488.1 GI:5940461
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AX284300
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HSA318881
HSA318880
AX226501
AC093664
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155851
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Copyright (c) 1993 - 2000 Compugen Ltd.
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PAT 29-SEP-1999

linear

tumor rejection antigen

107

160

BASE COUNT ORIGIN

Description

ID

Query Match Length DB

Score

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Result

180 180 240 240 300 420

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551 bp mRNA linear PRI 06-DEC-2001
G antigen 8, clone MGC:26395 IMAGE:4812462, mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Email: cgapbs-rémail.nih.gov
Email: cgapbs-rémail.nih.gov
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shirak
Toshhyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed Carninci (RIKEN)
DNA Sequencing Dy: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: (Dickson, Mark) mod@baxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submitted (03-DEC-2001) Mathemal Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                     AATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATT 480
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/organism="Homo sapiens"
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Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and
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2 (bases 1 to 530)
Van Den Eynde, B.J.
Direct Submission
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PATQRQDPAAAQEGEDEGASAGQGPRPEADSQEQGHPQTGCECEGEGGDEGDPPNPE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Lillie, J., Brown, J. L., Bolt, A. and van Huffel, C.
Novel genes, compositions and methods for the identification,
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                                                                                                                                                                                                           Score 533.2; DB 9;
Pred. No. 9.5e-119;
0; Mismatches 3;
/db_xref-"taxon:9606"
/clone-"MGC:26395 IMAGE:4812462"
/tissue_type-"Brain, hippocampus"
/clone_lib-"NHL MGC_95"
/lab_host-"DH10B"
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                                               /note="Vector: pBluescript" 97. .447
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99.48;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
Van den Eynde,B., Peeters,O., De Backer,O., Gaugler,B., Lucas,S.
and Boon,T.
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 of human cancers
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                                                                                                                                                           Score 531.6; DB 6;
Pred. No. 2.4e-118;
0; Mismatches 4;
assessment, prevention, and therapy of hu Patent: WO 0179556-A 827 25-OCT-2001; Millennium Predictive Medicine, Inc. (US) Location/Qualifiers
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                                                                      /organism="Homo saplens"
/db_xref="taxon:9606"
1 308 c 390 g 15
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                                                                                                                                                             Query Match
Best Local Similarity 99.3%;
Matches 534; Conservative
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U19143.1 GI:914900
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
De Backer, O., Arden, K.C., Boretti, M., Vantomme, V., De Smet, C.,
Czekay, S., Viars, C.S., De Plaen, E., Barsseur, F., Chomez, P., Van den
Eynde, B., Boon, T. and van der Bruggen, P.
Characterization of the GAGE genes that are expressed in various
human cancers and in normal testis
Cancer Res. 59 (13), 3157-3165 (1999)
                                                                                                                                                                                                                                                                                              /product-"GAGE-8"
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PATGRODPAAAGGEBDEGASAGGGFKPEADSQEGHPQTGCECEDGPDGQEMDPPNPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAA 191
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                                                                                                                                            2 (bases 1 to 528)
De Backer, O.R.Y.
Direct Submission
Submitted (24-MAR-1998) Ludwig Institute for Cancer Research,
Brussels Branch, 74 av. Hippocrate, Brussels B-1200, Belgium
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Pred. No. 7.3e-117;
0; Mismatches 1;
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Location/Qualifiers
1. 528
/organism="Homo sapiens"
/db_xref="taxon:9606"
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ilarity 99.8%;
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PATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPE
EVKTPEEGEKQSQC"
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       Submitted (28-DEC-1994) Benoit J Van Den Eynde, Ludwig Institute
For Cancer Research, 74 Avenue Hippocrate, BRUSSELS, 1200, BELGIUM
Location/Qualifiers
1. .530
/Organism="Homo sapiens"
/GD_xref="taxon:9606"
/sex="female"
/cell_line="M22-MEL.43"
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100.0%; Pred. No. 5.7e-118;
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                                                                                                                                                                         /product="GAGE-2 protein"
/protein_id="AAA82745.1"
/db_xref="GI:914901"
                                                                                                                  /tissue_type="melanoma"
/dev_stage="adult"
84. .434
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Best Local Similarity 100.
Matches 530; Conservative
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          29-SEP-1999
                                                                        Unclassified.

1 (bases 1 to 540)

van der Bruggen,P., van den Eynde,B., DeBacker,O. and
Boon-Falleur,T.
Isolated peptides derived from the gage tumor rejection antigen
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Pred. No. 8.2e-114;
0; Mismatches 7;
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Patent: US 5858689-A 16 12-JAN-1999;
Location/Qualiflers
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Sequence 16 from patent US 5648226.
155853.
155853.1 GI:2476647
         AR028490 540 bp
Sequence 16 from patent US 5858689.
AR028490
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                                      AR028490.1 GI:5940463
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Best Local Similarity 98.1%;
Matches 530; Conservative (
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Isolated peptides derived from the gage tumor rejection antigen precursor and uses thereof
Patent: US 5858689-A 18 12-JAN-1999;
Location/Qualifiers
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1 (bases 1 to 540)
Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and
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1 (bases 1 to 539)
van der Bruggen,P., van den Eynde,B., DeBacker,O. and
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llarity 98.1%; Pred. No. 8.2e-114;
Conservative 0; Mismatches 7;
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                                                          Patent: US 5648226-A 16 15-JUL-1997;
Location/Qualifiers
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Sequence 18 from patent US 5858689.
AR028492.1 GI:5940465
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113 c 157 a
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114 c 156 g
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179 180 239 419 420 479 480

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359 360

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Unclassified.

1 (bases 1 to 532)

van der Bruggen,P., van den Eynde,B., DeBacker,O. and
Boon-Falleur,T.

Isolated peptides derived from the gage tumor rejection antigen
precursor and uses thereof
Patent: US 585869-A 12-JAN-1999;
Location/Qualifiers
           CCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGT
                                                                 121 CCAAGGCGCTATGTACAGCCTCCTGAAGTGATTGGGCCTATGCGGCCCGAGCAGTTCAGT
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Pred. No. 7.1e-112;
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US 5858689.
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AR028491
AR028491.1 GI:5940464
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Van den Eynde, B., DeBacker, O. and Boon-Falleur, T.
Isolated peptides derived from tumor rejection antigens, and
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                                                                                                   TGAGATICATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGA
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smatches 8;
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llarity 98.0%; Pred. No. 3.5e-113;
Conservative 0; Mismatches 8;
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n tumor rejection antigens,
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Pred. No. 7.1e-112;
0; Mismatches 7;
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Van den Eynde,B., DeBacker,O. and Bool
Isolated peptides derived from tumor
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Location/Qualifiers
1. .532
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155854
155854.1 GI:2476648
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, 2.
Cancer gene determination and therapeutic screening using signature
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 4.7e-111
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98.3%; Pred. No. 4...
0; Mismatches
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4660 from Patent W00194629.
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Location/Qualifiers
1. 528
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mSwrgrstyywPrprryyQPPEMIGPMrPEQFSDEVEPATPEEG
EPATQRQDPAAAQEGEDEGASAGQGPKPEADSQEQGHPQTGCECEDGPDGQEMDPPNP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 528)
Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S.
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Pred. No. 4.7e-111;
0; Mismatches 6;
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/protein_id="AAA82747.1"
/db_xref="G1:914905"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="Mz2-MEL.43"
/tissue_type="melanoma"
/dev_stage="adult"
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Van Den Eynde, B.J.
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Best Local Similarity 98.3
Matches 518; Conservative
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REFERENCE
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2 (bases 1 to 527)
Van Den Eynde, B.J.
Direct Submission
Submitted (28-DEC-1994) BENOIT J VAN DEN EYNDE, Ludwig Institute
for Cancer Research, 74 Avenue Hippocrate, Brussels B-1200, Belgium
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mswrgrstyywprprrkyvoppevicpmrpeofsdevepatpegg|
Epatorodpaaaoegedegasagogprpeadsoeogegghpotgcecedgpogevdppnp
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Catarrhini; Hominidae; Homo.
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Van den Eynde, B., Peeters, O., De Backer, O., Gaugler, B., Lucas, S. and Boon, T.
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                                                   AGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGA
                                                                  359 TGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAA
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Pred. No. 2e-110;
0; Mismatches 7;
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/protein_id="AAA82749.1"
/db_xref="GI:914909"
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/db_xref="taxon:9606"
/sex="female"
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/tissue_type="melanoma"
/dev_stage="adult"
82. .435
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Mammalia; Eutheria; Primates;
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                                    TGAGATTCATCTGTGTGAATATGAGTTGGCGAGGAAGATCGACCTATTATTGGCCTAGA 120
                                                    CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
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Search completed: July 1, 2002, 07:13:58 Job time: 3733 sec

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538
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\*

em\_estba:\*
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Database :

	Description	BG700165 602679622	BG773070 602721370		BG250953 602363801	BG120838 602351010	BI868671 603392594	BM172302 imagegc_4	AA447559 zw81e11.s	AW510753 hd39d05.x	AI381509 te76b07.x	AA738037 nx15e11.s	BG700088 602679431	AW016546 UI-H-BIOP	BG120336 602353732	AA868226 ak48h07.s	AA760996 nx32h08.s	AI187350 qf29a05.x
SUMMARIES	ΙD	BG700165	BG773070	BI826605	BG250953	BG120838	B1868671	BM172302	AA447559	AW510753	AI381509	_		AW016546	BG120336	AA868226	AA760996	AI187350
	Length DB	569, 10	<b>b</b> 13 10	<b>5</b> 27 10	851 10	572 10	509 10	623 10	489 9	457 9	447 9		581 10		480 10	426 9	450 9	455 9
,	Query Match Lei	97.5	91.6	91.4	91.4	91.2	9.88	86.1	84.1	80.2	78.9	78.9	78.8	76.9	76.8	7.97	76.4	74.6
	Score	524.6	492.6	492	492	490.6	476.8	463.4	452.4	431.4	424.6	424.4	424	413.8	413.4	412.8	410.8	401.2
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## ALIGNMENTS

BG700165 569 bp mRNA linear EST 07-MAY-2001 602679622F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4812437 5', mRNA sequence. BG700165 BG700165.1 GI:13969233 EST. BG700165.1 GI:13969233 EST. BG700165.1 GI:13969233 EST.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  I (bases 1 to 569)  NIH-MGC http://mgc.nci.nih.gov/.  National Institutes of Health, Mammalian Gene Collection (MGC)  Contact: Robert Strausberg, Ph.D.  Email: cgapbs-r@mail.nih.gov  Contact: Robert Strausberg, Ph.D.  Email: cgapbs-r@mail.nih.gov  Contact: Robert Strausberg, Ph.D.  Contact: Robert Strausberg,	found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov Plate: LLAMIOOd row: 1 column: 06 High quality sequence stop: 566. Location/Qualiflers 1569 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Inamine"Homo sapiens" /clone="Inamine"Homo sapiens" /lissue_type="hippocampus" /lissue_type="hippocampus" /lab_host="DH10B" /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgap pluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (size-selected for average insert size 2: 5 kb and
RESULT 1 BG700165 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ODCANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES

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602721370F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4838176 5',
normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Garninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MSC Library."
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                     Score 524.6; DB 10;
Pred. No. 1e-111;
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TITLE
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527 bp mRNA linear EST 04-OCT-2001
Homo sapiens cDNA clone IMAGE:5168892 5',
                                                                                                                                                                                                                                    (gtcgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                           /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI: Site_2: SalI-XhoI (gtcg²); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 Lax benormalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the constructed using the constructed will be abownstein (MIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 GACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GTGATGAACTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAAGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 AAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 AAGCTGATAGCCAGGAACAGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 ATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 AGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 492.6; DB 10;
Pred. No. 2.8e-104;
0; Mismatches 14;
                                                                                                           1. .813
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4838176"
/clone_lib="NHH_MGC_97"
/lab_host="DH10B"
                                                                          ity sequence stop: 7
Location/Qualifiers
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603077056F1 NIH_MGC_119
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BI826605.1 GI:15938155
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96.8%;
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Matches 514; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: brain; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Ecorgan: brain; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Ecorga (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH-MGC Library."
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                                                  Euteleostomi;
                                                                                                                                                 Email: cgapbs-remain.inh.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LibMA1191 row: p column: 13
High quality sequence stop: 519.
Location/Qualifiers
//db_xref="taxon:9666"
//db_xref="taxon:9666"
//lone_lib="mAndE:516892"
//lone_lib="mandEd:19"
//lab.host="mandEd:19"
//lab.host="mandEd:19"
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoo
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 492; DB 10;
Pred. No. 3.8e-104;
0; Mismatches 5;
                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 91.4%;
al Similarity 98.3%;
519; Conservative
                                Homo sapiens
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Best Local S
Matches 519
                               ORGANISM
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ORIGIN
                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
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/organism="Homo sapiens"
/organism="Homo sapiens"
/organism="Homo sapiens"
/olone="IMAGE:471969"
/clone=lib="NHIH_MGC_90"
/clone=lib="NHIH_MGC_90"
/tissue_type="denocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a 183 t 183 t
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                                               124 GACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATG
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                                                                                                                                                                                                                                     Score 492; DB 10;
Pred. No. 3.9e-104;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BG250953
BG250953.1 GI:12760769
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Best Local Similarity 96.4%;
Matches 515; Conservative
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/clone="IMAGE:4445882"
/clone="IMAGE:4445882"
/clone=Ltype="adenocarcinoma, cell line"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: liver; Vector: pCWV-SpoRT6; Site_1: NotI;
/note="organ: liver; Vector: liver; Vec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG120838 572 bp mRNA linear EST 30-JAN-2001 602351010F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4445882 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapps-remail.nih.gov
Tissue Procurement: AFCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the INA MG.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10224 row: c column: 03
High quality sequence stop: 572.
Location/Qualifiers
I. 572
//organism="Homo sapiens"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 572)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                   430
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CTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGGAGCCTGAAGCTC 303
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                         AGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAAT
                                                                                                                                                                                                                                          CACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGT
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Pred. No. 8.1e-104;
0; Mismatches 14; Indels
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BG120838
BG120838.1 GI:12614347
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Best Local Similarity 96.7
Matches, 523; Conservative
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603392594F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402663 5', mRNA sequence.
B1868671
B1868671.1 G1:16042344
EST.
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E 1 (bases 1 to 509)

National Institutes of Health, Mammalian Gene Collection (MGC)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

High quality sequence stop: 509.

Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                            387
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                                                                     238 CTGCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTG
                                                                                                                                                                                                                                                                                            298 AAGCICATAGCCAGGAACAGGGICACCCACAGACTGGGIGIGAGTGTGAAGAIGGICCIG
                                                                                                                                                                                                                                                                                                             /tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_90"
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                                          Technologies
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                          Length 509;
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                                                                                                                             DB 10;
                                                                                                                          Score 476.8; DB 10;
Pred. No. 1.3e-100;
0; Mismatches 7;
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Lawrence Livermore National Laboratory
Livermore, CA, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 623)
Kale, P.I., Harsch, T.J., Folta, P.A.,
Prange, C.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The I.M.A.G.E. Consortium quality resequencing for verification Unpublished (2001)
Other_ESTs: BG773070
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98.08;
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Email: help@image.llnl.gov

This read has been verified (found to hit its original self in the correct orientation), as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact info@image.llnl.gov.

Seq primer: -21ml3
                                                                                                                                                                                                                                                                                                                               pBluescript KS+); Site_1: BamHF; Site_2: Sall-Xhoi (gtcga Size-selected for average insert size_2: Z kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the constructed using the constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.
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                                                                                                                                                                                                                                                                                /clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 463.4; DB 1
Pred. No. 1.7e-97;
); Mismatches 26
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/db_xref="taxon:9606"
/clone="IMAGE:4838176"
                                                                                                                                                                                    High quality sequence stop: 623.
Location/Qualifiers
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Best Local Similarity 94.5%;
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(bases 1 to 489)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

Unpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782636 to TR:G914905 G914905 GAGE-4 PROTEIN. [1];, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                         Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fex: 314 286 1810
Email: est@watson.wustl.edu
Fins clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 427.
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Pred. No. 6e-95;
0; Mismatches 6; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_testis_NHT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:782636"
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                                                                                                AA447559.1 GI:2161229
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Best Local Similarity 98.0%;
Matches 480; Conservative
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Best Local Similarity
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                                                                                                                             human.
                                        DEFINITION
RESULT 8
AA447559/c
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KEYWORDS
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Another Corgan: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCL_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726468-728711, and 729096-731399, Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW510753 457 bp mRNA linear EST 03-MAR-2000 hd39d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2911881 3' similar to SW:GGE4_HUMAN Q13068 GAGE-4 PROTEIN. ; AW510753
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Contact: Robert Strausberg, Ph.D.
Contact: Copbrt Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                     519
CGCCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAG 459
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Pred. No. 4.5e-90;
); Mismatches 6;
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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    .457
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 447)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 497 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI381509 447 bp mRNA linear EST 28-MAR-te76b07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092597 3' similar to TR:Q13070 Q13070 GAGE-6 PROTEIN.;
                                                                                                                                                                                                                                                                  217 ACAGGGTCACCCACAGAGTGTGAGTGTGAGTGTGAGATGGTCCTGATGGCAGGAGGAGGATGGA 158
                                                                                                                                                                                                                                                                                                                         397 ACAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACC 338
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              AGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACC
                                                                                                               194 AGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTCAGGA
                                                                                                                                                                    254 GGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:21092597"
/clone_lib="Scares_NFL_T_GBC_S1"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 TCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGAAA 530
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AI381509
AI381509.1 GI:4194290
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Contact: Robert Strusberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 511 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 435.
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1 (bases 1 to 464)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                     268
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                                                                                                                                                                         145 AAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTG 204
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                                               3,
      Length 447;
                                               Indels
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    6
  Score 424.6; DB 9
Pred. No. 1.7e-88;
0; Mismatches 4
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Best Local Similarity 98.4%;
Matches 440; Conservative
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581 bp mRNA linear EST 07-MAY-2001 602679431F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4812462 5', mRNA sequence.
BG700088
BG700088.1 GI:13969078
                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                     /note="Wector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I -oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Scares and M. Fatima Bonaldo. " 132 c 93 g 153 t
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1 (bases I to 581)
NHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
                                                                                                                                                                                                                                                                                                                                                                                              84 ATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGACGCTACGTAGAGCCT 140
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                                                                                                                                                                                                                                                                                                                               464;
                                                                                                                                                                                                                                                                                                                         78.9%; Score 424.4; DB 9; Length 96.9%; Pred. No. 1.9e-88; Ive 0; Mismatches 11; Indels
                               /clone="IMAGE:1256204"
/clone_lib="NCI_CGAP_GG3"
/tissue_type="pooled germ cell tumors"
/lab_nost="DH108"
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                /db_xref="taxon:9606
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                                                                                                                                                                                                                                                                                                                     Length 581;
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                                                                                                                                                                                                                                                                                                                   Score 424; DB 10;
Pred. No. 2.4e-88;
0; Mismatches 30;
                                                                                                               1. .581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4812462"
/clone_lib="NIH_MGC_95"
                                                                                             High quality sequence stop: 548.
Location/Qualifiers
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Best Local Similarity 92.8%;
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1 (bases 1 to 418)

1 (bases 1 to 418)

1 (bases 1 to 418)

1 (App http://www.ncbi.nlm.nih.gov/ncicgap.

1 (App ncer Institute, Cancer Genome Anatomy Project (CGAP), Contact: Robert Strausberg, Ph.D.

2 (Contact: Robert Strausberg, Ph.D.

2 (Contact: Robert Strausberg, Ph.D.

3 (Contact: Robert Strausberg, Ph.D.

3 (Contact: Robert Strausberg, Ph.D.

4 (Appl.) (Appl
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MINA linear EST 10-SEP-1999 UI-H-B1D9-abg-g-06-0-UI.S1 NCI_CGAP_SUb2 Homo sapiens cDNA clone IMAGE:2711986 3', mRNA sequence.
AW016546.1 GI:5865303
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/db_xref="taxon:9606"
/clone="IMAGE:2711986"
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ORIGIN
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/lab_host="DH108 (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 Rb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG120336 480 bp mRNA linear EST 30-JAN-
602353732F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451958 5′
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMI0239 row: p column: 07
High quality sequence stop: 480.
                                                                                                                                                                                                                                                                                        122 AAGACGCTACGTAGAGCCTCCTGAAATGATTGGGGCCTATGCGGCCCGAGCAGTTCAGTGA 181
                                                                                                                         299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                             182 TGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGC 241
                                                                                                                                                                                                                                                                                                                                                                                      302 TCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCA 421
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       Length 418;
                                                     Indels
76.9%; Score 413.8; DB 9;
99.5%; Pred. No. 5.5e-86;
tive 0; Mismatches 2;
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/clone="IMAGE:4451958"
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BG120336.1 GI:12613845
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information can be
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
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                                                                                                                                                                  GAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGGAACCAGCAACTCAA
                                                                                                                                                                                                                   GATGGTCCTGATGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAA
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                                                                                 ;
                                                       Length 480;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                  Indels
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                                                       DB 10;
                                                       Score 413.4; DB 1
Pred. No. 6.8e-86;
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                                                                                 0; Mismatches
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  133
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                                                    Query Match 76.8%;
Best Local Similarity 97.4%;
Matches 420; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      162 CGGCCCGAGCAGTTCAGTGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                       222 ACTCAACGTCAGGATCCTGCAGCTGCTCAGGAGGGAGGATGAGGGAGCATCTGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 CAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 TGTGAAGATGGTCCTGATGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 CCTGAAGAAGGTGAAAAGCAATCACAGTGTTAAAAAGAAGACACGTTGAAATGATGCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 TGCTCCTATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTG
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                                                                                                                                                                                                                                                                                     76.7%; Score 412.8; DB 9;
llarity 97.9%; Pred. No. 9.4e-86;
Conservative 0; Mismatches 9;
                                       /clone_lib="Soares_testis_NHT"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                           /clone="IMAGE:1409245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, 2002, 06:39:18
                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 417; Conserv
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Job time: 1653 sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 1, 2002, 06:11:45; Search time 201.18 Seconds (without alignments) 4591.411 Million cell updates/sec Run on:

US-09-782-745-14 538 1 ACGCCAGGGAGCTGTGAGGC.......CTGCAAAGAAAAAAAAA 538 Title: Perfect score:

Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3472872 Total number of hits satisfying chosen parameters: 1736436 segs, 858457221 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_032802:\* Database :

| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:\*
| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:\*
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| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1992.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	GAGE-2 tumour reje	Human cancer agent	GAGE-4 tumour reje	GAGE-6 tumour reje	GAGE-5 tumour reje	cDNA encoding GAGE	cDNA encoding GAGE	cDNA encoding GAGE	cDNA encoding GAGE
SUMMARIES		Ω		AAS60826	AAX90521	AAX90523	AAX90522	AAV18721	AAV18720	AAV18717	AAV18719
		DB	20	22	20	20	50	19	19	19	19
		Query re Match Length DB 1	538	1245	540	540	532	539	532	535	541
	æ	Query Match	100.0	98.8	95.3	94.8	93.8	93.0	92.3	91.6	91.2
		Score	538	531.6	512.8	510.2	504.8	500.6	496.8	493	490.6
		Result No.	-	7	m	4	വ	9	7	80	5

GAGE-3 tumour rejectonA encoding GAGE Human prostate can Human prostate can GAGE tumour reject CAGE tumour reject CAGE tumour reject Human secreted pro Human secreted pro	secreted a cancer a cancer a cancer a polynuch polynuch polynuch polynuch polynuch polynuch prostate cell cyc cell cyc nooding a nooding	Human polynucleoti Human NOV3 DNA. H Human secreted pro Human lung tumour Human lung tumour DNA encoding novel Human secreted pro Human prostate cDN Human prostate-spe Prostate tumour an Human ovarian PCR- Human ovarian PCR- Human ovarian tumo CSG Prol18 EST use
AAX90520 AAV18718 AAZ97216 AAT31861 AAX90518 AAV05540 AAC07129	AAC01129 AAS60104 AAS60104 AAI58744 AAI14983 AAS69484 AAZ97402 AAS69486 AAV05532 AAC5532	AAK52902 AAH64798 AAH64798 AAF68861 AAF68151 AAS91235 AAS91235 AAS913316 AAH93807 AAH95121 AAH95121 AAH9337 AAH83260 AAH83260
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## ALIGNMENTS

Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic T lymphocyte; GAGE; ss. GAGE-2 tumour rejection antigen clone nucleotide sequence. AAX90519 standard; cDNA; 538 BP (first entry) WO9937665-A1. Homo sapiens. 30-SEP-1999 AAX90519; RESULT AAX90519 

99WO-US00775. 12-JAN-1999; 29-JUL-1999.

(LUDW-) LUDWIG INST CANCER RES.

98US-0012818.

23-JAN-1998;

Van Der Bruggen P; œ, Boon-Falleur T, Debacker O, Van Den Eynde

New isolated peptides which bind to HLA-A29 molecules, which are tumour rejection antigens used for detection and therapy of

WPI; 1999-469111/39.

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                                                The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLS) in pathological conditions such as cancer and in HLA-Typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
Lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATT 480
                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCTGCTCAGGAGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAG
                                                                                                                                                                                                                                                               ACGCCAGGGAGCTGTGAGGCAGTGCTGTGTTTCCTGCCGTCCGGACTCTTTTTCCTCT
                                                                                                                                                                                                                                                                                                                   ACTGAGATTCATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACCTATCGGCCTAGAC
                                                                                                                                                                                                                                                                                                                                                                     CAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGGCCTATGCGGCCCCGAGCAGTTCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                    cagctgctcaggaggagaggatgagggagcatctgcaggtcaagggccgaagcctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                       Sequence 538 BP; 160 A; 116 C; 155 G; 107 T; 0 other;
                                                                                                                                                                                                          100.0%; Score 538; DB 20; 100.0%; Pred. No. 3e-146;
                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer agent-sensitive marker #328
pathological conditions, e.g. cancer
                           Example 13; Fig 4; 62pp; English,
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocytic leukaemia; lymphom
Hodgkin's disease; glioma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS60826 standard; cDNA; 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                     Matches 538; Conservative
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002
                                                                                                                                              invention.
                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                           Local
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The invention relates to 1046 novel nucleic acids which are used as markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown not to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL.

The methods can be used to determine the effectiveness of TAXOL.

The methods can be used to determine the effectiveness of TAXOL.

The methods can be used to determine the effectiveness of TAXOL.

The methods can be used to determine the effectiveness of TAXOL.

The methods can be used to determine the effectiveness of TAXOL.

The methods can be used to determine the markers can also be used as targets in developing treatments for cancer, particularly those cancers which alsolate cancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), imphonma, plasmocytoma, reticulum cell sarcona, Hodgkin's disease and turnors (e.g. gliona), the present sequence is one of the 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the effectiveness of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 acgccagggagctgtgaggcagtgctgtgtgtggttcctgccgtccggactctttttcctct 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid, used as a marker to determine the e
using TAXOL to treat cancer cell growth in individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1245 BP; 382 A; 308 C; 390 G; 153 T; 12 other
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                                                                                                                                                                                                                                                                                                                                                                  Van Huffel C;
                                                                                                                                                                                                                                                                                           MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 340; 527pp; English.
                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE
                                                                                                                                                                                                                                                                                                                                                                  Bolt A,
                                                                                                                                          13-APR-2001; 2001WO-US12132
                                                                                                                                                                                                                14-APR-2000; 2000US-197538P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer cell markers.
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Best Local Similarity
WO200179556-A2.
                                                                      25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                  Lillie J,
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WPI; 1999-469111/39.
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                                                                                                                                                                                                                                                                                                                                 30-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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AAX90523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic Tlymphocytes (CTLS) in pathological conditions such as cancer and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAGATTCATCTGTGTAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAG 118
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Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCAGGGAGCTGTGAGGCAGTGCTGTGGGTTCCTGCCGTCCGGACTCTTTTTCCTTA
                             AATCACAGTGTTAAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATT
                                                                                                                                                                                                                                                                                                                                                                      Van Der Bruggen
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m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                          New isolated peptides which bind to HLA-A29 molecules, which tumour rejection antigens used for detection and therapy of
                                                                                                                                                                                                              Human leukocyte antigen; HLA-A29; tumour rejection antigen;
detection; therapy; pathological condition; cancer; CTL;
cytolytic T lymphocyte; GAGE; ss.
                                                                                                                                                                                            GAGE-4 tumour rejection antigen clone nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 540 BP; 159 A; 114 C; 156 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 512.8; DB 20;
Pred. No. 6.2e-139;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                       Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                             pathological conditions, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                      Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Fig 4; 62pp; English.
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(0
                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                  AAX90521 standard; cDNA; 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.3%;
                                                                                                                                                                                                                                                                                                              99WO-US00775
                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   Boon-Falleur T,
                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                       W09937665-A1
                                                                                                                                                                                                                                                                                                              12-JAN-1999;
                                                                                                                                                                        30-SEP-1999
                                                                                                                                                                                                                                                                                          29-JUL-1999.
                                                                                                                                                     AAX90521;
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          539
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The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLS) in pathological conditions such as cancer and in HLA-Typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                           418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
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AGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGGTGTGAAGATGGTCCTGA
                                                                                                                                                                                                                                                                                                                 GCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGA
                                                                                                                                                                                                                                                                                                                                                                                         TGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAA 
                                                                                                                                                                                                               New isolated peptides which bind to HLA-A29 molecules, which are tumour rejection antigens used for detection and therapy of pathological conditions, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; HLA-A29; tumour rejection antigen;
detection; therapy; pathological condition; cancer; CTL;
cytolytic T lymphocyte; GAGE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGE-6 tumour rejection antigen clone nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Den Eynde
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                    gccagggagctgtgaggcagtgctgtgtggttcctgccgtccggactcttttcctctac
                                                                                                                                                           gatgaagtggaaccagcaacatctgaagaaggggaaccagcaactcaacgtcaggatcct
                                                                                                                                                                         GCAGCTGCTCAGGAGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAA
                                                                                                                                                                                                      GCTCATAGCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGGTGGAAGATGGTCCTGAT
                                                                                                                                                                                                                                    GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAG
                                                                                                                                                                                                                                           CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT
                                                                                                                CCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGT
                                                                                                                                            GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT
                                                                                                                                                                                                                                                                                            Der Bruggen
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3;
                       540;
                       Length
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                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; HLA-A29; tumour rejection antig
detection; therapy; pathological condition; cancer; CTL;
cytolytic T lymphocyte; GAGE; ss.
 other;
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                      Score 510.2; DB 20;
Pred. No. 3.6e-138;
0; Mismatches 8;
0
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 Ξ.
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 G; 111
C; 157
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98.0%;
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113
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                             Local Similarity 98.0 tes 528; Conservative
                                                                                                                                                                                                                                                                                                                                                  cDNA;
 Ä,
BP; 159
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                      Query Match
Best Local Si
Matches 528
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antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                   present invention describes peptides which bind to human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
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                                                                                                                                                                                                                                                                                                                                                                      10 AGCTGTGAGGCAGTGCTGTGTGTGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATT
                                                                                                                                                                                                                                                                                                                                                                                      CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTACGTAGAGCCTCCTGAAATGATTGGCCCTATGCGGCCCCGAGCAGTTCAGTGATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCAGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agtgttaaaaagaaaggcacgttgaaatgatgcaggctgctcctatgttggaaatttgttca
   are
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                                                                                                                                                                                                                                                                                                     532;
 which
                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding GAGE-6 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                    BP; 156 A; 111 C; 154 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                  Score 504.8; DB 20;
Pred. No. 1.3e-136;
0; Mismatches 7;
                                 pathological conditions, e.g. cancer
peptides which bind to
lon antigens used for
                                                                    English.
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llarity 98.1%;
Conservative
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                                                                  Fig 4; 62pp;
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 522; Conserv
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                   rejection
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   isolated
                                                                    Example 13;
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                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                        Seguence
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AAV18721
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AAV18720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 GCAGCTGCTCAGGAGGAGAGATGAGGGAGCATCTGCAGGTCAAGGCCGAAGCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 CCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCGAGCAGTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ccaaggcactatgtacagcctcctgaagtgattgggcctatgcggcccgagcagttcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 GATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCT
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                                                                                          aa:Arg)
aa:Ala)
aa:Thr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.2e-135, 0; Mismatches 14,
                                                                         /*tag= a //transl_except= (pos:127..129, /transl_except= (pos:196.198, /transl_except= (pos:199..201,
                                                                                                                                                                                                                                                                                                    Van Den Eynde B;
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                                             Location/Qualiflers
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                                                                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES
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                 sapiens
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The present sequence encodes a GAGE-5 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV1817-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE connex for the first 112 bases. This region of GAGE-3 cona contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by
                                                             360
                                                                                            419
                                                                                                     241 gcagotgotcaggaggaggaggatgagggagcatotgcaggtcaagggccgaagcotgaa 300
                                                                                                                                                   CAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAAT 479
                                                                                                                                                                                                                538
                                                                                                                                                                                                                            GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation; HLA-typing assay; ss.
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                           360 GGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAG
                                                                                                                                                                                                           cDNA encoding GAGE-5 tumour rejection antigen precursor.
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aa:Thr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_except= (pos:189..191, /transl_except= (pos:192..194,
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                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                    AAV18720 standard; cDNA; 532
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P-PSDB; AAW47602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnose melanomas
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23-JUN-1997;
                                                 24-JUN-1996;
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hes 524;
          31-DEC-1997
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                                          transplants
expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants
                                                                                                                                                  1 agctgtgaggcagtgctgtgtggttcctgccgtccggactctttttcctctactgagatt
                                                                                                                                                                                                             GCTACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATGAAG
                                                                                                                                                                                                                                                             CTCAGGAGGAGGAGGATGAGGGGGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGGTCATA
                                                                                                                                                                                                                                                                                                              ctcaggaggaggaggatgagggagcatctgcaggtcaagggccgaagcctgaagctgata
                                                                                                                                                                                                                                                                                                                                                                                            agatggacccgccaaaatccagaggaggtgaaaacgcctgaagaaggtgaaaagcaatcac
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                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTGTGAGGCAGTGCTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTACTGAGATT
                                                                                                                                                                      CATCTGTGTGAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAGACCAAGAC
                                                                                                                                                                                                                                                    TGGAACCAGCAACACTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTG
                                                                                                                                                                                                                                                                                                                                  GCCAGGAACAGGGTCACCACACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGG
                                                                                                                                                                                                                                                                                                                                                      gccaggaacagggtcacccacagactgggtgtgagtgtgaatgatggtcctgatgggcagg
                                                                                                                                                                                                                                                                                                                                                                         AGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCAC
                                                                                                                                                                                                                                 ggtatgtacagcctcctgaagtgattgggcctatgcggcccgagcagttcagtgatgaag
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                                                                                         DB 19; Length 532;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aa:Ala)
aa:Thr)
                                                            Sequence 532 BP; 154 A; 110 C; 156 G; 112 T; 0 other
                                                                                                            12;
                                                                                        Score 496.8; DB 19,
Pred. No. 2.7e-134;
0; Mismatches 12;
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/transl_except= (pos:192..194,
./transl_except= (pos:195..197,
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                                                                                        92.3%;
ilarity 97.2%;
Conservative 0
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                                                                                                   Best Local Similarity
Matches 517; Conser
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contrast the only normal tissue which expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPS have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequences not the rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 DNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic 7 cell clone proliferation methodologies. Other uses for the processed peptides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence encodes a GAGE-2 tumour tumour rejection antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     include HLA-typing assays for, e.g. skin graft or organ transplants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACTGAGATTCATCTGTGTGAGATATGAGTTGGCGAGGAGGAGGACGACCATCGGCCTAGA
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                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful diagnose melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.6%; Score 493; DB 19;
llarity 97.2%; Pred. No. 3.5e-133;
Conservative 0; Mismatches 10;
                                                                                                                                                                                                       B,
                                                                                                                                                                                                       Van Den Eynde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Fig 4; 60pp; English.
                                                                                                                                   (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                       Debacker O,
                                                               96US-0669161
97WO-US10850
                                                                                                                                                                                                                                                                          WPI; 1998-076905/07.
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                                                                                                                                                                                                                                                                                                       P-PSDB; AAW47599
                                                                                                                                                                                                       Boon-Falleur T,
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5

5

Gaps

4;

Indels

14;

0; Mismatches

Conservative

523;

Matches

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The present sequence encodes a GAGE-4 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the CAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants.
               caatcacagtgttaaaaagaagacatgttgaaatgatgcaggctgctcctatgttggaaat 476
                                               Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas
                                                                                                                                                                                                                                                                                                       GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation; HLA-typing assay; ss.
cDNA encoding GAGE-4 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/transl_except= (pos:197..199, aa:Ala)
/transl_except= (pos:200..202, aa:Thr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boon-Falleur T, Debacker O, Van Den Eynde B;
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                     BP.
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                                                                                                                                                                     AAV18719 standard; cDNA; 541
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               417
                                                                                477
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ID AAV1
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Length 541;

Score 490.6; DB 19; Pred. No. 1.8e-132;

91.2%; 96.7%;

Query Match Best Local Similarity

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240
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                                                                                                                                                                                                                                                                                                                     537
                                     CTGAGATTCATCTGTGTAAATATGAGTTGGCGAGGAAGATCGACC---TATCGGCCTAG 118
                                                         120
                                                                             178
CGCCAGGGAGCTGTGAGGCAGTGCTGTGTGGTTCCTGCCGTCCGGACTCTTTTTCCTCTA 61
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                                                                                                                    TGATGAAGTGGAACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCC
                                                                                                                                       181 tgatgaagtggaaccagagcctcctgaagaaggggaaccagcaactcaacgtcaggatcc
                                                                                                                                                                                                                                         TGGGCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAAACGCCTGAAGAAGGTGAAAA
                                                                                                                                                                                                                                                    AGCTCATAGCCAGGAACAGGGTCACCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGA
                                                                                                                                                                                                                                                                                 419 GCAATCACAGTGTTAAAAGAAGACACGTTG-AAATGATGCAGGCTGCTCCTATGTTGGAA
                                                                                                                                                           TGCAGCTGCTCAGGAGGGAGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Der Bruggen
                                                                                                                                                                                                            Human leukocyte antigen; HLA-A29; tumour rejection antigen; detection; therapy; pathological condition; cancer; CTL; cytolytic I lymphocyte; GAGE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGE-3 tumour rejection antigen clone nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX90520 standard; cDNA; 560 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US00775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Homo sapiens

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                                                                                       The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into Lumnour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLs) in pathological conditions such as cancer and in HLA-typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLs in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                 168
                                                                                                                                                                                                                                                                                                                                  TCTTTTTCCTCTACTGAGATTCATCTGTGAAATATGAGTTGGCGAGGAAGATCGACCT 108
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                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              ATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGGCCTATGCGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 agcagttcagtgatgaagtggaaccagcaacactgaagaaggggaaccagcaactcaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTCCTGATGGGCAGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 atgttggaaatttgttcattaaaattctcccaataaagctttacagccttctgcaaagaa
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                                                                                                                                                                                                                                                                          Length 560;
isolated peptides which bind to HLA-A29 molecules, which
                 rejection antigens used for detection and therapy of
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding GAGE-3 tumour rejection antigen precursor.
                                                                                                                                                                                                                            Sequence 560 BP; 177 A; 119 C; 150 G; 114 T; 0 other;
                                                                                                                                                                                                                                                                         Score 429.2; DB 20;
Pred. No. 1.2e-114;
                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                       0; Mismatches
                              pathological conditions, e.g. cancer
                                                         Example 13; Fig 4; 62pp; English.
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                                                                                                                                                                                                                                                                       79.8%;
92.2%;
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Best Local Similarity 92.2
Matches 452; Conservative
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                                                                                                                                                                                              invention.
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contrast the only normal tissue which expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is nested to only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 (AAV05540) is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAs for the first 112 bases. This region of GAGE-3 contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to proliferation methodologies. Other uses for the processed peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a GAGE-3 tumour tumour rejection antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tegteetegecaacteatattteacacagatgaateteagtagaggaaaategaeetatt 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 ATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGGCCTATGCGGCCCG 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      include HLA-typing assays for, e.g. skin graft or organ transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 attggcctagaccaaggcgctatgtacagcctcctgaagtgattgggcctatgcggcccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid encoding GACE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.3%; Score 421.2; DB 19; Length 560; 91.2%; Pred. No. 2.6e-112;
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                                                                              aa:Ala)
aa:Thr)
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                                                                          (pos:217..219, (pos:220..222,
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                                Location/Qualifiers
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                                                             /*tag= a
/transl_except=
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                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
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447; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     diagnose melanomas
                                                                                                                                                                                                                                                                                        Boon-Falleur T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a prostate cancer specific nucleic acid sequence. The invention relates to a method for diagnosing cancer, tumour progression, hyperproliferative cell growth or accompanying biological and physical manifestations. The method involves contacting the biological sample with a probe that comprises a sequence capable of hybridising to any of the 339 nucleotide sequences given in the products and methods of the invention can be used for the diagnosis, prognosis, and treatment of cancer, tumour progression, hyperproliferative cell growth, and accompanying physical and biological manifestations. They can be used particularly for prostatic disorders such as metastatic prostate cancer, localised prostate cancer, or benign
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to develop
                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer specific gene; cancer; tumour progression; diagnose; hyperproliferative cell growth; prostatic disorder; treatment; metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
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                                                                                                            469 ATGTTGGAAATTTGTTCATTAAAATTCTCCCAATAAAGCTTTACAGCCTTCTGCAAAGAA
 ATGGTCCTGATGGCCAGGAGATGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAG
                                                                   371 atggtcctgatgggcaggagatggacccgccaaatccagaggaggtgaaaacgcctgaag
                                                      409 AAGGTGAAAAGCAATCACAGTGTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE,
                                                                                                                                                                                                                                                                                                                                              Human prostate cancer differentially expressed gene #78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated prostate cancer specific nucleic acids, fucts for the diagnosis and treatment of cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ford DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 107; 212pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endege WO,
                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                             AAZ97217 standard; cDNA; 1024
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                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-116541/10.
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                                                                                                                                                                                529 AAAAAAAAA 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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09-JUN-1999;
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Length 1024;

399.4; DB 21; No. 7.3e-106;

Score Pred.

74.2%;

Query Match Best Local Similarity

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This sequence represents a prostate cancer specific nucleic acid sequence. The invention relates to a method for diagnosing cancer, tumour progression, hyperproliferative cell growth or accompanying biological and physical manifestations. The method involves contacting the biological sample with a probe that comprises a sequence capable of
130 ACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCCGAGCAGTTCAGTGATGAAGTGG 189
                                                   249
                                                                            219
                                                                                                     309
                                                                                                                               279
                                                                                                                                                          369
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                          aggtacagcctcctgaaatgattgggcctatgcggcccgagcagttcagtgatgaagcgg 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer specific gene; cancer; tumour progression; diagnose; hyperproliferative cell growth; prostatic disorder; treatment; metastatic prostate cancer; benign prostate hyperplasia; BPH; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated prostate cancer specific nucleic acids, used to develop lucts for the diagnosis and treatment of cancer \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlegel
                                                                                                                                                                                                                                                                            AACCAGCAACACCTGAAGAAGGGGAACCAGCAACTCAACGTCAGGATCCTGCAGCTGCTC
                                                                                                        AGGAGGGAGGATGAGGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCC
                                                                                                                      310 AGGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGATGGTCCTGATGGGCAGGAGA
                                                                                                                                                                                                             TGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGT
                                                                                                                                                                                                                                                               GITAAAAGAAGACACGITGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTGTTCATTA
                                                                                                                                                                                                                                                                                                                   Monahan JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate cancer differentially expressed gene #77.
                                                                                                                                                                                                                                                                                                                                 DW,
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99US-0088877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Astel JH, Carroll E, Steinmann KE, Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-116541/10.
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21-SEP-1995;
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hybridising to any of the 339 nucleotide sequences given in the specification (see AA297140-297478) and detecting duplex formation. The products and methods of the invention can be used for the diagnosis, prognosis, and treatment of cancer, tumour progression, hyperproliferative cell growth, and accompanying physical and biological manifestations. They can be used particularly for prostatic disorders such as metastatic prostate cancer, localised prostate cancer, or benign prostate hyperplasia (BPH).
                                                                                                                                                                                          249
                                                                                                                                                  130 ACGTAGAGCCTCCTGAAATGATTGGGCCCTATGCGGCCCGAGCAGTTCAGTGATGAAGTGG 189
                                                                                                                                                            402
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                                                                                                                                                                                                                                                                                                                       222
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                                                                                                                                                                                                                           AGGAGGGAGAGGATGAGGAGCATCTGCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCC
                                                                                                                                                                                                                                     370 TGGACCCGCCAAATCCAGAGGAGGTGAAAACGCCTGAAGAAGGTGAAAAGCAATCACAGT
                                                                                                                                                                                                                                                                                                             GTTAAAAGAAGACACGTTGAAATGATGCAGGCTGCTCCTATGTTGGAAATTTTGTTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGE gene; tumour rejection antigen; TRA; precursor; TRAP; human; melanoma cell line; HLA-A29 molecule; binding peptide; diagnosis; cancer; typing assay; skin graft; organ transplant; MHC; major histocompatibility complex; ss.
                                                                                                                 Length 1024;
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0
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                                                                                   Sequence 1024 BP; 187 A; 290 C; 232 G; 270 T; 45 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "putative open reading frame"
                                                                                                                DB 21;
                                                                                                               Score 397.4; DB 21;
Pred. No. 2.8e-105;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGE tumour rejection antigen precursor gene
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49..469
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                                                                                                              73.9%;
98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                             Query Match 73.9
Best Local Similarity 98.0
Matches 401; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 cctatgcggcccgagcagttcagtgatgaagtggaaccagcaacacctgaagaaggggaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is GAGE tumour rejection antigen (TRA) precursor (TRAP) gene, derived from the human melanoma cell line MZ2-MEL (see PCT/US92/O4154). It encodes peptides that are processed into human MHC HLA-A29 mol. binding peptides, i.e. TRA. The TRA peptides can be used in the diagnosis of pathological conditions, e.g. cancer, and for carrying out HLA-typing assays, e.g. for skin grafts or organ transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 CIGCCGICCGGACTCTTTTCCTCTACTGAGATTCATCTGTGTGAAATATGAGTTGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 GCAGGTCAAGGGCCGAAGCCTGAAGCTCATAGCCAGGAACAGGGTCACCCACAGACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 TGTGAGTGTGAAGATGGTCCTGATGGCCAGGAGATGGACCCGCCAAATCCAGAGGAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 646;
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detection; therapy; pathological condition; cancer; CTL;
cytolytic I lymphocyte; GAGE; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                Der
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGE tumour rejection antigen clone nucleotide sequence.
                                                                                                                                                                      Isolated tumour rejection antigen genes and peptide(s) develop prods. for diagnosis and treatment of abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 646 BP; 188 A; 140 C; 174 G; 144 T; 0 other;
                                                                                                Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 374.4; DB 1
Pred. No. 1.1e-98;
0; Mismatches 1
                                                                                                В,
                                                                                                Den Eynde
                                                                                                Van
                                                                                                                                                                                                                                                   Example 6; Page 43; 61pp; English.
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                                                        (LUDW-) LUDWIG INST CANCER RES
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ilarity 99.7%;
Conservative
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                  95US-0370648.
95US-0531662
                                                                                                Debacker
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                                                                                                                                  WPI; 1996-342237/34.
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                                                                                              Boon-Falleur
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Homo sapiens

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                                                                                                                                                                                                                                                                          The present invention describes peptides which bind to human leukocyte antigen (HLA) A29 (HLA-A29) molecules. The peptides are processed into tumour rejection antigens. They can be used for detecting cytolytic T lymphocytes (CTLS) in pathological conditions such as cancer and in HLA-Typing assays. Complexes of HLA-29 molecules and the peptides can be used for stimulating CTLS in vivo. The present sequence represents a GAGE tumour rejection antigen clone, from an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAAGATCGACCTATCGGCCTAGACCAAGACGCTACGTAGAGCCTCCTGAAATGATTGGG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van Der Bruggen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTATGCGGCCCGAGCAGTTCAGTGAAGTGGAACCAGCAACACCTGAAGAAGGGGGAA
                                                                                                                                                                                                   New isolated peptides which bind to HLA-A29 molecules, which are tumour rejection antigens used for detection and therapy of pathological conditions, e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Length 646;
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Pred. No. 1.1e-98;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 646 BP; 188 A; 140 C; 174 G; 144 T; 0 other;
                                                                                                                                                   Van Den Eynde B,
                                                                                                                                                                                                                                                    Example 9; Page 38; 62pp; English
                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                   Boon-Falleur T, Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 69.6%;
Best Local Similarity 99.7%;
Matches 375; Conservative
                                                                                                  98US-0012818
                                                                          99WO-US00775
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                                                                                                                                                                           WPI; 1999-469111/39
                       WO9937665-A1
                                                                        12-JAN-1999;
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Search completed: July 1, 2002, 06:44:03 Job time: 1938 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 1, 2002, 06:29:18 ; Search time 14.38 Seconds (without alignments) 775.130 Million cell updates/sec

US-09-782-745-27 646 1 MSWRGRSTYRPRPRRYVEPP......DPPNPEEVKTPEEGEKQSQC 116 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	probable immediate	glutamate/proline-	glutamate/proline-	proline-rich prote	proline-rich prote	surface protein rh	proline-rich phosp	glutenin high mole	glutenin, high-mol	~	glutenin high mole	calcium binding 14	calcium-binding pr	proline-rich prote	hypothetical prote	OmpA family protei	beta-conglycinin a	hypothetical prote	zinc metalloprotei	proline-rich prote	neurofilament trip	beta-conglycinin a	NF-180 - sea lampr		glutenin, high mol			salivary proline-r	tegument protein 6
SUMMARIES	ID	T03166	S70010	S70009	E29149	S22373	A58938	A27307	B30843	JN0689	S15720	S02262	PC4014 .	T30282	S19560	B97586	AC2807	FWSYBA	F96531	Н95076	S10889	OFPGL	S20007	151116	B36298	EEWTHW	T34073	T51023	B25372	S55659
	DB				7																									
	Length	1300	139	221	301	260	396	171	815	812	830	848	652	1560	300	754	754	902	847	1881				1110	212	838	1606	2649	166	3436
ď	Ouery Match	18.4	17.0	17.0	16.4	16.3	16.1	16.0	15.9	15.9	15.9	15.9	15.8	15.8	15.7	15.6	15.6	15.6	15.6	15.5	15.4	15.4	15.4	15.4	15.2	15.2	15.2	15.2	15.1	15.1
	Score	119	110	110	106	105.5	104	103,5	102.5	102.5	102.5	102.5	102	102	101.5	101	101	100.5	100.5	100	99.5	99.2	99.5	99.5	86	86	86	86	97.5	97.5
	Result No.	-	7	m	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

proline-rich prote E4 protein - human actin-binding prot	neurofilament trip neurofilament prot zinc metalloprotei	neurofilament trip matrix glycoprotei proline-rich prote	hypothetical proce hypothetical prote spalt-related prot E4 protein - human	salivary proline-r hypothetical prote acidic proline-ric
A39066 W4WL8 S42719	OFMSL JW0094 E97944	S07144 GERTX1 A36298	14882/ T20980 T13805 W4WL5	PIHUSD T16324 PIRT3
242	1444	2212	7007	177
204 229 617	543 554 1876	544 634 220	183 1263 245	310 325 206
000	نامون	مقوة	4.4.6 6.6.6 5.6.6	₹. c. 4.
15 14	14	7777	1444	14
97 96.5 96.5	96	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	94.5 94 93.5	93.5 93.5 93
30 31 32		38 38 38 38	2444 2010 2010	4 4 4 6 4 5

## ALIGNMENTS

RESULT 1 102166 probable immediate early protein - alcelaphine herpesvirus 1 C;Species: alcelaphine herpesvirus 1 C;Species: 124-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999 C;Date: 70: 6517-6525, 1997 A;Title: Primary structure of the alcelaphine herpesvirus 1 genome. A;Reference number: 214840; MUID:97404659 A;Accession: T03166 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1300 <ens> A;Residues: 1-1300 <ens> A;Cross-references: EMBL:AF005370; NID:92337967; PIDN:AAC58118.1; PID:92338034 C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal hom</ens></ens>
Query Match 18.4%; Score 119; DB 2; Length 1300; Best Local Similarity 35.2%; Pred. No. 0.18; Matches 45; Conservative 7; Mismatches 44; Indels 32; Gaps 7;
OY 17 VEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGE 59 1
Qy 60 DEGASAGQEPKPEAHSQEOGHPQTGCECEDGPDGQEMDPPNPEEVKT 106
Qy 107 PEEGEKQS 114              bb 646 P-EGECQS 652
RESULT 2 Sy0010 glutamate/proline-rich protein (clone BB.1.4.1) - rat C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Accesion: S70010 R.Geertman, R.; McMahon, A.; Sabban, E.L. Biochim. Biophys. Acta 1306, 147-152, 1996 A.Title: Cloning and characterization of cDNAs for novel proteins with glutamic ach A.Reference number: S70009; MUID:96221285 A.Accession: S70010 A.Status: preliminary A.Molecule type: MRNA A.Residues: 1-139 cGEB> A.Cross-references: EMBL:040628; NID:g1184695; PIDN:AAB05668.1; PID:g1184696

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A; Molecule type: mRNA
A; Residues: 1-396 <BOO>
A; Cross-references: GB:M71274; NID:g897822; PIDN:AAA69859.1; PID:g897823
A; Note: revision to sequence reported in A45644
R; Ossorio, P.N.; Schwartzman, J.D.; Boothroyd, J.C.
MOI. Biochem. Parasitol: 50, 1-15, 1992
A; Title: A Toxoplasma gondii rhoptry protein associated with host cell penetratic
A; Reference number: A45644; MUID:92178277
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A;Accession: A45644
A;Accession: AASACARCLLCSVQNLLFFFLRDIYCTDFDT',1-352,'FPQR',358-364,'R',366,'I',393,'A;Residues: 'MACRQLLCSVQNLLFFFLRDIYCTDFDT',1-352,'FPQR',358-364,'R',366,'I',393,'A;Cross-references: EMBL:M71274; NID:g897822
A;Cross-references: EMBL:M71274; NID:g897822
A;Note: sequence extracted from NCBI backbone (NCBIN:85178, NCBIP:85179)
                                                                                                                                                                                                                                                                                                                                  mRNA regulation by
                                                                                                                                                                                               Cipecies: Mus musculus (house mouse)
Cipecies: Mus musculus (house mouse)
Cipecies: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
Cincesion: 222373 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
Riayfield, R.; Bannister, A.J.; Pierce, E.J.; McDonald, C.J.
Eur. J. Biochem. 204, 591-597, 1992
A.Title: CDNA clones for mouse parotid proline-rich proteins. mRNA regulatic
A; Reference number: S22373; MUID:92174915
A; Reference number: S22373
A; Mould a mouse parotid proline-rich proteins
A; Residues: 1-260 < LAX>
A; Residues: 1-260 < LAX>
A; Cross-references: EMBL:X63004; NID:953798; PIDN:CAA44733.1; PID:953799
C; Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Toxoplasma gondii
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A58938; A45644; S37697
R; Boothroyd, J.C.
submitted to GenBank, July 1995
A; Reference number: A58938
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 PRPGNQQEPPPQGGPQFPSRPGNQQGP--PPQGGP--QQRPP---QPGNQQGPPPQGGPQ 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 -- PEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 GGPQPGRNQGFPPQGGPQRPRGNQQFPPPQGGPQRPPQPGNHQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      surface protein rhoptry ROP1 precursor - Toxoplasma gondii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.3%; Score 105.5; D
29.5%; Pred. No. 0.4;
iive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: surface protein rhoptry C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Matches 40; Conservative
                                                                                                                                                                                    - mouse
          101 PEEVKTPEEGEKQ 113
                                                      234 GGPOGPPRPGNQQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 31; Conserv
                                                                                                                                                                               proline-rich protein
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Best Local Si
Matches 31;
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                                                                                                                                                                                                                                                                                                                                                            glutamate/proline-rich protein (clone 53.1.1.1) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S70009
R:Geertman, R.; McMahon, A.; Sabban, E.L.
Blochim. Biophys. Acta 1306, 147-152, 1996
A:Title: Cloning and characterization of cDNAs for novel proteins with glutamic acid-pro
A:Accession: S70009
A;Actaus: preliminary
A;Actaus: preliminary
A;Residues: 1-221 <GEE>
A;Cross-references: EMBL:U40627; NID:g1184693; PIDN:AAB05667.1; PID:g1184694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proline rich protein - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Musrugeg #sequence_revision 08-Mar-1989 #text_change 20-Aug-1999
C; Accession: E29149
R; Clements, S.; Mehansho, H.; Carlson, D.M.
J. Biol. Chem. 260, 13477-13477, 1985
A; Title: Novel multigene familise encoding highly repetitive peptide sequences. Sequence A; Contents: Clone pUMP125
A; Contents: Clone pUMP125
A; Coccession: E29149
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-301 < CLE>
A; Coss references: GB:M1897; NID:9200540; PIDN:AAA40001.1; PID:9200541
C; Superfamily: proline-rich protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 GASAG-----QGPKPEAHSQ-----EQGHPQTGCECEDGPDG-----QEMDPPN 100
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 QGSSQQRPPQPGQPPPQGGPQQRPPQPGNQQGP--PPPGGPQQRPPQPGGNQGPPPQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                          15 RYVEPPEMIGPMRPEQFSDEVEPATPEGGE---PATQRQDPAAAQEGEDEGASAGQGPKP 71
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                                                      22;
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     Length 139;
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                                                   Indels
                                                                                                                                                                                                                              72 EAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTP--EEGEKQSQC 116
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                                              15; Mismatches
  Score 110;
                            Pred. No.
17.0%;
31.8%;
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     Local S...
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Matches 34;
  Query Match
                    Best Loc
Matches
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Am. J. Hum. Genet. 41, 1035-1047, 1987
A.Title: Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich paracession: A27307; MUID:88074309
A; Reference number: A27307; MUID:88074309
A; Accession: A27307
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-171 < AZE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutenin high molecular weight chain Ax2 precursor - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 15-Nov-1996
                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 29-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 AQEGE----DEGASAGQGPKPEAHSQEQG--HPQTGCECEDGPDGQEMDPPNPE---EV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 EQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAG------QGPKPEAHSQEQG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 EQFLDEERQGPPLGG----QQSQPSAGDGNQDDGPQGGQQQGQQQQGP-PPPQGKPQG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SWRGRSTYRPRPRRYVEPPEMIG------PMRPEQFSDEVEPATPEGGEPATQRQDPAA 54
60 4. - DEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGE 111
                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 171;
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                                                                                                                                       proline-rich phosphoprotein (gene PRHI, Db allele) - human N.Alternate names: salivary acidic proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: B30843
R; Anderson, O.D.; Greene, F.C.
submitted to GenBank, January 1989
A; Reference number: A94515
A; Accession: B30843
A; Molecule type: DNA
A; Residues: 1-815
A; Residues: 1-815
C; Superfamily: glutenin
C; Superfamily: glutenin
C; Superfamily: signal sequence #status predicted <SIG>F; 1-21/Domain: signal sequence #status predicted <AMAF; 22-815/Product: glutenin Ax2 chain #status predicted <MAF; 108-773/Region: glutamine/glycine/proline-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 103.5; D
Pred. No. 0.39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:119515; OMIM:168730
A;Map position: 12p13.2-12p13.2
S:Superfamily: proline-rich protein
C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.0%;
30.9%;
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Glutenin, high-molecular-weight Ax2* chain precursor - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 14-101-1994 #sequence_revision 14-Jul-1994 #text_change 15-Nov-1996
C;Accession: JN0689
R;Anderson, O.D.; Greene, F.C.
Theor. Appl. Genet. 77, 689-700, 1989
A;Title: The characterization and comparative analysis of high-molecular-weight g
A;Reference number: JN0689
A;Accession: JN0689
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-815 <AND>
A; Note: the authors translated the codon CTA for residue 11 as Val, CAT for residue 5; Comment: The main wheat storage proteins are divided into two groups. The gluter c; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Triticum aestivum (common wheat)
C;Date: 08-Jun-1994 #sequence_revision 12-May-1995 #text_change 20-Aug-1999
C;Accession: S15720
R;Halford, N.G.; Field, J.M.; Blair, H.; Urwin, P.; Moore, K.; Robert, L.; Thomps:
Submitted to the EMBL Data Library, July 1991
A;Description: Analysis of HWW glutenin subunit encoded by chromosome 1A of bread
A;Reference number: S15720
A;Accession: S15720
A;Actaus: preliminary
A;Molecule type: DNA
A;Residues: 1-830 cHAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Gene: Ax2*
C;Superfamily: glutenin
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-815/Product: glutenin, high-molecular-weight Ax2* chain #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X61009; NID:g21742; PIDN:CAA43331.1; PID:g21743
C;Superfamily: glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWRGRSTYRPRPRRYVEPPEMIG------PMRPEQFSDEVEPATPEEGEPATQRQDPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 AQEGE----DEGASAGQGPKPEAHSQEQG--HPQTGCECEDGPDGQEMDPPNPE---EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.9%; Score 102.5; E
Best Local Similarity 23.7%; Pred. No. 1.9;
Matches 31; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%; Score 102.5; 24.0%; Pred. No. 2; ive 20; Mismatches
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105 KTPEEGEKQSQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 KTPEEGEKQSQ 115
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Best Local Similarity
Matches 31; Conserv
                                 1 : 1 : 1 480 480 00PAQGQPGQ
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A;Title: Gene sequence of mouse B-type proline-rich protein MP4. Transcriptional A;Reference number: S19560; MUID:92111548
A;Accession: S19560
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R:Roberts, S.G.E.; Layfield, R.; McDonald, C.J.
Nucleic Acids Res. 19, 5205-5211, 1991
A):Title: The mouse proline-rich protein MP6 promoter binds isoprenaline-inducibl
A)Reference number: S22570; MUID:92020206
                                                                                                                           C; Species: Strongylocentrotus purpuratus (purple urchin)
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C; Accession: T30282
R; Soltysik-Espanola, M.; Klinzing, D.C.; Pfarr, K.; Burke, R.D.; Ernst, S.G. Dev. Biol. 165, 73-85, 1994
A; Title: Endol6, a large multidomain protein found on the surface and ECM of A; Reference number: 220805; MUID:94374583
A; Reference number: 220805; MuID:94374583
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proline-rich protein MP4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C:Accession: S19560; S22570
R:Roberts, S.G.E.; Layfield, R.; Bannister, A.J.; McDonald, C.J.
Bur. J. Biochem. 202, 969-974, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1362 EVKTSNQEGSEVQEESQDPQEQMEGEGQG-SESEGEEPEGEGG-PQEQVESEGEENE 1419
                                                                                                                                                                                                                                                                                                                                                                                          A;CTCoss-references: EMBL:L34680; NID:g511893; PID:g511894; PIDN:AAA30047.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QGSSQQRPPQPGNQQGPPPQGGPQQRPPQPGNQQGP--PPPGGPQQRPPQPGGNQGGPPQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GA-----SAGOGPKPEAHSQ-----EQGHPQTGCECEDGPD-----GQEMDPPNP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCPHPPPRPGNQGFPPQGGPQQRPTQPGNQGFPQQG-----GPQAPPRPGNQGFPPQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                           purpuratus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 EVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.8%; Score 102; DB 2; Length 1560; 32.0%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                      calcium-binding protein - sea urchin (Strongylocentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | : | | | : | | | : 1420 SEEEEVEEPEGEQQVMESEGQQSESEEPEFEGEEPEESEGEQE 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DGP-----DGQEMDPPNPE-EVKTPEEGEKQSQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
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Best Local Similarity 28.8%; Pred. No. 0.91;
Matches 38; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 3.8;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:X61126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  1-1560 <SOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-300 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-14 <RO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S22570
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: endo16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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S19560
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                                                                                                                                                                                                               Sultenin high molecular weight chain Dx5 - wheat
C;Species: Triticum aestivum (common wheat)
C;Species: Triticum destivum (common wheat)
C;Species: Sreb-1994
C;Species: Sol262
R;Anderson, O.D.; Greene, F.C.; Yip, R.E.; Halford, N.G.; Shewry, P.R.; Malpica-Romero, Nucleotide sequences of the two high-molecular-weight glutenin genes from the IA; Reference number: Sol262; MuID:89098419
A;Reference number: Sol262; MuID:89098419
A;Residues: 1-848 <AND>
A;Residues: 1-848 <AND>
A;Residues: 1-848 <AND>
A;Coss-references: EMBL:X12928
C;Genetics: Clu-11
C;Superfamily: glutenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium binding 140k protein - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 21-7u1-1995$ #sequence_revision 31-Mar-1997 #text_change 05-Nov-1999
C; Accession: Pc4014
R; Naved, A.F.; Ozawa, M.; Yu, S.; Miyauchi, T.; Muramatsu, H.; Muramatsu, T.
Cell; Struct. Funct. 20, 133-141, 1995
A; Title: CBP-140, a novel endoplasmic reticulum resident Ca2+-binding protein with a ca: A; Reference number: PC4014; MUID:95368740
A; Title: CBP-140, a novel endoplasmic reticulum resident Ca2+-binding protein with a ca: A; Reference number: PC4014
A; Molecule type: mRNA
A; Residues: 1-652 < NNAV
A; Cross references: GB:S78797; NID:91041986; PIDN:AAB35051.1; PID:91041987
A; Cross references: GB:S78797; NID:91041986; PIDN:AAB35051.1; PID:91041987
C; Comment: The sequence 1-80 has high homology to that of 70k heat shock protein
C; Keywords: calcium binding: endoplasmic reticulum; heat shock; stress-induced protein
F; 649-652/Region: endoplasmic reticulum retention signal #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 GQQGQQPGQGEQGQQPGQQQQQQQQQPGYYPTSPQQSGQGQPGYYPTSPQQSGQLQQ 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RGRSTYRP------RPRRYVEPPE-----MIGPMRPEQFS---DEVEPATPEEGE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGE--DEGASAGQGPKPEAHSQEQGHPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 102.5;
Pred No. 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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by/obthetical protein AGR_C_3445 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens C; Date C; Dat
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15.6%; Score 101; DB 2; Length 754;
Best Local Similarity 27.7%; Pred. No. 2.3;
Matches 36; Conservative 15; Mismatches 47; Indels 32; Gaps
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234 GPOGPPRTGNQQ 245
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_40:\* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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RESULT

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-!- TISSUE SPECIFICITY: EXPRESSED IN SOME PROSTATE CANCER TISSUES BUT NOT IN NORMAL PROSTATE TISSUE.
-!- SIMILARITY: BELONGS TO THE GAGE FAMILY.
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MEDILTRE-98116329; PubMed=9651357;
MEDILTRE-98116329; PubMed=9651357;
Chen M.E., Lin S.-H., Chung L.W.K., Sikes R.A.;
"Isolation and characterization of PAGE-1 and GAGE-7: new genes expressed in the LINCaP prostate cancer progression model that share thomology with melanoma-associated antigens.";
J. Biol. Chem. 273:17618-17625(1998).
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammafia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Backer O.R.Y.;
"Structure, chromosomal location and control of expression of the GAGE genes.";
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nllarity 97.4%; Pred. no. 9.68-37;
Conservative 1; Mismatches 1; Indels 1.
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1; Indels
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                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) GAGE-7 protein (G antigen 7) (GAGE-8) (AL4).
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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(Rel. 39, Last anno
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                                       STANDARD;
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SEQUENCE FROM N.A.
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AC 013068;
DT 15-JUL-1998
DT 30-MAY-2000
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                                                                                                                                                          "A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma.";
J. Exp. Med. 182:689-698(1995).
--- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR TISSUES BUT NOT IN NORMAL TISSUES. EXCEPT TESTIS.
--- SIMILARITY: BELONGS TO THE GAGE FAMILY.
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J. Exp. Med. 182:689-698(1985).
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR TISSUES BUT
NOT IN NORMAL TISSUES, EXCEPT TESTIS.
-!- SIMILARITY: BELONGS TO THE GACE FAMILY.
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Usukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                    van den Eynde B., Peeters O., de Backer O., Gaugler B., Lucas S.,
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MEDLINE-95378788; PubMed-7544395;
van den Eynde B., Peeters O., de Backer O., Gaugler B., Lucas S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family.
SEQUENCE 117 AA; 12956 MW; 365ED71B2F9DC7AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 616.5; DB 1;
Pred. No. 3.9e-36;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) GAGE-5 protein (G antigen 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                TISSUE=Melanoma;
MEDLINE=95378788; PubMed=7544395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.4%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U19145; AAA82747.1; -.
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Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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   SEQUENCE FROM N.A.
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Q13069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                        Boon T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGES.
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GGE5_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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RESULT 7
GGE3_HUMAN
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                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boon T.;
"A new family of genes coding for an antigen recognized by autologous cytolytic T lymphocytes on a human melanoma.";
J. Exp. Med. 182:689-698(1995).
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR TISSUES BUT NOT IN NORMAL TISSUES, EXCEPT TESTIS.
-!- SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSWRGRSTYR-PRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGE 59
                                                                                                                                                                                                                                      MSWRGRSTYR-PRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGE 59
                                                                                                                                                                                                                                                                  DEGASAGOGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 DEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC 116
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Melanoma;
MEDLINE-95378788; PubMed-7544395;
van den Eynde B., Peeters O., de Backer O., Gaugler B., Lucas S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 608.5; DB 1; Length 117; Pred. No. 1.4e-35; Mismatches 2; Indels 1
                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234A865E3FCCCD06 CRC64;
            MIN; 604247; -.
Multigene family.
eronFNCE 117 AA; 12924 MW; 234A865E2ECDDD06 CRC64;
                                                                                                                                       Score 612.5; DB 1;
Pred. No. 7.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA; 12892 MW;
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                                                                                                                                       94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGE-6 protein (G antigen 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.95
Matches 111; Conservative
EMBL; U19146; AAA82748.1;
                                                                                                                                       Query Match
Best Local Similarity 95.77
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family. SEQUENCE 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 604248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGE6_HUMAN
Q13070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGE6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
GGE6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TESTIS.
--- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR TISSUES BUT NOT IN NORMAL TISSUES, EXCEPT TESTIS.
--- SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostom1;
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ISSUB-Machanoma;
MEDLINE-95378/R8; PubWed=7544395;
van den Eynde B., Peeters O., de Backer O., Gaugler B., Lucas S.,
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                      van den Eynde B., Peeters O., de Backer O., Gaugler B., Lucas S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family; Antigen.
SEQUENCE 138 AA; 15418 MW; 37BBF3909EC4B3B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 598; DB 1;
Pred. No. 8.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGE3_HUMAN STANDARD; PRT; 118 AA. Q13067; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JMAY-2000 (Rel. 39, Last annotation update) GAGE-3 protein (G antigen 3).
                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-JUL-1998 (Rel. 39, Last annotation update)
GAGE-1 protein (G antigen 1) (MZ2-F antigen).
138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                              TISSUE=Melanoma;
MEDLINE=9537878; PubMed=7544395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U19142; AAA82744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.6'
Best Local Similarity 99.1'
Matches 108; Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604243
                                                                                                                                                                                                                                                                                                                                                               Boon T.;
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MIM; 300288; -. Multigene family

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXPRESSION ASSOCIATED WITH PROGRESSION TO ANDROGEN INSENSITIVE PHENOTYPE. EXPRESSED IN NORMAL TESTIS AND AT LOWER LEVEL IN NORMAL
                          genes coding for an antigen recognized by autologous hocytes on a human melanoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                    Cytolytic T lymphocytes on a human melanoma.";
J. Exp. Med. 182:689-698(1995).
-1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TUMOR TISSUES BUT
NOT IN NORMAL TISSUES, EXCEPT TESTIS.
-1- SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98316329; PubMed-9651357;
Chen M.E., Lin S.-H., Chung L.W.K., Sikes R.A.;
"Isolation and characterization of PAGE-1 and GAGE-7: new genes
expressed in the LNCaP prostate cancer progression model that share
homology with melanoma-associated antigens.";
J. Biol. Chem. 273:17618-17625(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RGRSTYR-PRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGBL. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: ISOLATED FROM PROSTATE CANCER CELL LINES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Multigene family.
SEOUENCE 118 AA; 12937 MW; D97EEBB19E735103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 589.5; DB 1;
Pred. No. 2.7e-34;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF058989; AAC25990.1; -
                                                                                                                                                                                                                                                                                                                                                                   EMBL; U19144; AAA82746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 91.3%;
Local Similarity 94.7%;
les 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
Boon T.;
"A new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLACENTA
                                                                                                                                                                                                                                                                                                                                                                                              604245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGB1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
  δλ
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                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                      ----- GPKPEAHSQEQ 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "PAGE-1, an X chromosome-linked GAGE-like gene that is expressed in normal and neoplastic prostate, testis, and uterus."; Proc. Natl. Acad. Sci. U.S.A. 95:10757-10762(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEMALE REPRODUCTIVE TISSUES, PROSTATE, TESTIS, FALLOPIAN TUBE, UTERUS, AND PLASCENTA, AS WELL AS IN PROSTATE CANCER, TESTICULAR CANCER, AND UTERING CANCER.
-!- SIMILARITY: BELONGS TO THE GAGE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Strom T.M., Nyakatura G., Hellebrand H., Drescher B., Rosenthal A.,
                                                                                                                                                                              1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGED
                                                                                                                                                                                                                             1 MGFLRRLIYRRRPMIYVE----SSEESSDE----QPDEVESPTQSQDSTPAEERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
G antigen family C 1 protein (Prostate-associated gene protein 4)
GAGE-4) (PAGE-1) (JM27) (GAGE-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-98393718; PubMed-9724777;
Brinkmann U., Vasmatzis G., Lee B., Yerushalmi N., Essand M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN NORMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
16134 MW; 91ABA1E3B498DCA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AA; 11153 MW; CE5D07AFBF73301B CRC64;
                                                                         Score 266; DB 1; I
Pred. No. 3.2e-12;
7; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                 109 VHPKTGCERGDGPDVQELGLPNPEEVKTPEEDEGQSQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 120; DB 1;
Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA.
                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      79 GHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQ
                                                                                                                                                                                                                                                                                   EGASAGO-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF275258; AAF88037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                            41.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ005894; CAA06751.1;
EMBL; AF238380; AAF62541.1;
MIM; 300287; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.6%;
34.5%;
                                                                                                  Similarity 42.0 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human).
146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGC1_HUMAN
O60829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pastan I.;
SEQUENCE
                                                                            Query Match
                                                                                                       Best Local
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         ä
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HARDON CELL. BIOL. 6:1965-1973(1986).

-I- ALTERNATIVE PRODUCTS: DROSOPHILA TROPOMYOSIN 1 GENE CAN PRODUCE FOUND LIFEREBRY I SOPROMS BY ALTERNATIVE PRODUCTS: A MUSCLE FORM, AND TWO FUSION PROPEINS (33 AND 34).

-I- DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.

-I- SIMILARITY: BELOAGGS TO THE TROPOMYOSIN FAMILY.

-I- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN MAINLY BECAUSE OF ALTERNATIVE EXON USAGE.
           Gaps
                                          1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGED 60
                                                              "The Drosophila melanogaster tropomyosin II gene produces multiple proteins by use of alternative tissue-specific promoters and alternative splicing.";
Mol. Cell. Biol. 8:3591-3602(1988).
         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karlik C.C., Fyrberg E.A.;
"Two Drosophila melanogaster tropomyosin genes: structural and
                                                                                                                                EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coiled coil; Repeat; Alternative splicing; Multigene family.

14 275 COILED COIL (POTENTIAL).

DOMAIN 298 504 ALA/PRO-RICH.
         52; Indels
                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
         Mismatches
                                                                                                                                                                                                                                       504 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X76208; CAA53801.1; -.
EMBL; L00362; AAA28965.1; -.
EMBL; M12840; AAA28965.1; -.
EMBL; L00355; AAA28965.1; JOINED.
EMBL; L00355; AAA28965.1; JOINED.
EMBL; L00356; AAA28965.1; JOINED.
EMBL; L00357; AAA28965.1; JOINED.
EMBL; L00358; AAA28965.1; JOINED.
FLYBASE; FB970003721; Tml.
                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE OF 1-286 FROM N.A.
MEDLINE-87064486; Pubmed=3097506;
                                                                                                                                                                                                                                                                                                                     Tropomyosin 1, fusion protein 34.
TM1 OR TMII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-89127197; Pubmed-2851721;
Hanke P.D., Storti R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00194; TROPOMYOSIN.
PROSITE; PS00326; TROPOMYOSIN; 1.
         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00261; Tropomyosin;
Matches 39; Conservative
                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  functional aspects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-7227;
                                                                                                                                                                                                                                       TPM5_DROME
                                                                                                                                                                                                                                                         P49456;
                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 15:197-201(1990).

-!- FUNCTION: SEED STORAGE PROTEIN. ACCUMULATES DURING SEED
DEVELOPMENT AND IS HYDROLYZED AFFER SERAITION TO PROVIDE A
CARBON AND NITROGEN SOURCE FOR THE DEVELOPING SEEDLING.
-!- SUBUNIT: THE ALPHA'-, ALPHA-, AND BETA-SUBUNITS ASSOCIATE IN
VARIOUS COMBINATIONS TO FORM TRIMERIC PROTEINS.
-!- SUBCELLULAR LOCATION: EMBRYO AXIS, AND COTYLEDONARY MEMBRANE-BOUND
VACUOLAR PROTEIN BODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Core eudicots; Rosidae;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

NCBI_TaxID-3847;
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                            15 RYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQCPKPEAH 74
                     A -> S (IN REF. 2).
A -> MVEADLERAERA (IN REF. 2).
V -> L (IN REF. 2).
NOREEEVKNOIKTLNTR -> TQKEETFETQIKVLDHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA-CONGLYCININ, ALPHA CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CBEBBA30506BBBC57 CRC64;
                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE 7S SEED STORAGE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sebastiani F.L., Farrel L.B., Schuler M.A., Beachy R.N.; "Complete sequence of a cDNA of alpha subunit of soybean beta-
                                                                                                                                                                                                                        Score 100.5; DB 1; Length 504; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seed storage protein; Signal; Glycoprotein; Multigene family.
SASAIQLAA (IN REF.
                                                                                                                                                                                                                                                                          42; Indels
                                                                                                                            (IN REF. 2).
642C5D73F03AAC43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 14, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä
                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 GAAPGEPGAATE----PGVEAPPAEPERIPTP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                 75 SQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTP 107
  LGSATAKLS ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-conglycinin, alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: X17698; CAA35691.1; --
PIR; S14681; FWSYBA.
HSSP: P50477; 1CAU.
InterPro; IPR001113; Seedstore_7s.
Pfam; PF00546; Seedstore_7s; 1.
Pfam; PF02808; Seedstore_7s_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Cotyledon;
MEDLINE-91355860; PubMed-2103438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70293 MW;
                                                                                                                                                      MW.
                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.3%;
Matches 31; Conservative
                                                                                                                                                 504 AA; 53634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
62
605
261
517
  1114
1119
1183
1199
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63
261
517
605 AA;
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106
119
183
199
215
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01-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLCA_SOYBN
P13916;
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CARBOHYD
CARBOHYD
SEQUENCE
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Geisler N., Kaufmann E., Fischer S., Plessmann U., Weber K.;

"Neurofilament architecture combines structural principles of
"netendiate filaments with carboxy-terminal extensions increasing
in size between triplet proteins.";

EMBO J. 2:1295-1307(1983).

"I- FUNCIION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NURONAL CALLBER.

"I- FUNCIION: NEUROFILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT
PROTEINS ARE DUE TO THE TAILPIECE EXTENSIONS. THIS REGION MAY FORM
COTHER NEUROMAL COMPONENTS OR IONS.

A CHARGED SCAFFOLDING STRUCTURE SUITABLE FOR INTERACTION WITH
PROTEINS NEURONAL COMPONENTS OR IONS.

OTHER NEURONAL COMPONENTS OR IONS.

MISCELLANBOUS: NF-L IS THE MOST ABUNDANT OF THE THREE

NEUROFILAMENT PROTEINS, IT CAN FORM HOMOPOLYMERIC 10-NM
                                                                                                                                                                                                                                                                                75 RPRPR-----PQHPER----EPQQPGEKEEDEDEQPRPIPFPRPQPRQEEEHEQ 119
                                                                                                                                                                                                                                               63 ASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMD-----PPNPEEVKTPEEGEKQS 114
                                                                                   Gaps
                                                                                                                                         62
                                                                                                                             10 RPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQD-----PAAAQEGEDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-02T-1996 (Rel. 34, Last sequence update)
16-02T-2001 (Rel. 40, Last annotation update)
Neurofilament triplet L protein (68 kDa neurofilament protein)
(Neurofilament light polypeptide) (NF-L).
                          Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY. PIR; A02963; QFFGL.
INTERPO; IFF001664; IF.
PFGM: PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Glycoprotein.
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geisler N., Plessmann U., Weber K.; "The complete amino acid sequence of the major mammalian
                          DB 1;
                                                                                40;
548 AA.
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COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
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LINKER 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurofilament protein (NF-L).";
FEBS Lett. 182:475-478(1985).
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
395
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     Query Match
Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                             115 0 115
                                                                                                                                                                                                                                                                                                                                                                                                                      175 Q 175
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NFL_PIG
ID NFL_PIG
AC P02547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE
PROTEIN OF WHEAT ENDSPERM: THOUGHT TO BE RESPONSIBLE FOR THE
VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-!- SUBMUNT: DISULETIDE-BRIDGE LINKED AGGREGATES.
-!- KISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
GROUP 1 CHROMOSOMES OF WHEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 GRSAYGGLQTSSYLMSTRSFPSYYTSHVQEEQIEVEETIEAAKAEEAKDE-PPSEGEAEE 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 PATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequences of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GRSTY------RPRPRRY----VEPPEMIGPMRPEQFSDEVEPATPEEGE 44
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Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GOOPGO AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STAIN-EV. CHEYENNE;
MEDLINE-89098419; PubMed=2563152;
Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R.,
Malpica-Romero J.M.;
                             TAIL, SUBDOMAIN A.
TAIL, SUBDOMAIN B (ACIDIC).
O-LINKED (GLCNAC) (BY SIMILARITY).
O-LINKED (GLCNAC) (BY SIMILARITY).
EPITOPE (RECOGNIZED BY IF-SPECIFIC MONOCLONAL ANTIBODY).
                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                              Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit DX5 precursor.
GLU-1D-1D OR GLU-D1-1B.
                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                           15.4%; Score 99.5; DE 26.2%; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative
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548 AA;
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P10388;
DOMAIN
DOMAIN
DOMAIN
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CARBOHYD
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SEQUENCE
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Best Local S
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PRINTS; PR00210; GLUTENIN.
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide P-C
                                                                                                                                                                                                                                                                                                                                                                                              PRPC_HUMAN
                                                                               SEQUENCE
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                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                      551 QPGQLQQPAQGQQGQQLAQGQQGQQPAQVQQGQQPAQGQQGQQLGQGQQGQQ--PGQGQQ 608
                                                                                                                                                                                                                                                                               491 QGQPGYYPTSPQQSGQGQQPGQWQQPGQGQPGYYPTSPLQPGQGQPGYDPTSPQQPGQGQ 550
                                                                                                                                                                                                                                                                                                            45 PATORODPAAAQEGED-EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
61 cutenin, high molecular weight subunit PW212 precursor.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                     4 RGRSTYRP------RPRRYVEPPE-----MIGPMRPEQFS---DEVEPATPEEGE 44
                                                                                                             GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUCCELC ACIÓS RES. 13:8729-8737(1985).

"UCCELCA ACIÓS RES. 13:8729-8737(1985).

"UCCELCA ACIÓS RES. 13:8729-8737(1985).

PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.

"I SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES.

"INSCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF GROUP I CHROMOSOMES OF WHEAT.

"I SATURE PRATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GOOPGQ AND
                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. YAMHILL;
MEDLINE-86038674; PubMed-3001648;
Suglyama T., Rafalski A., Peterson D., Soll D.G.;
"A wheat HMW glutenin subunit gene reveals a highly repeated
                                                                                                                                                                                              15.3%; Score 99; DB 1; Length 839; 23.5%; Pred. No. 3.3; tive 22; Mismatches 57; Indels
                                                                                    Seed storage protein; Repeat; Multigene family; Signal. SIGNAL \ 1\ 21
                                                                                                                                                        OF14E1106D552643 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    838 AA
 send an email to license@isb-sib.ch).
                                                                                                                                         REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                       PIR; S02262; S02262.
InterPro; IPR001419; Glutenin.
PRINTS; PR00210; GLUTENIN.
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InterPro; IPR001419; Glutenin
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89359 MW;
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                             EMBL; X12928; CAA31395.1; -.
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                839
                                                                                                                                                                                                                                                                                                                                                                    104 VKTPEEGEKQSQ 115
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609 GOOPAQGQGGQ 620
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                                                                                                                                          131 8
839 AA;
                                                                                                                                                                                                             Best_Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLT4_WHEAT
ID GLT4_WHEAT
AC P08489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure.
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                                                                                                                                                                                                   Query Match
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556 QPGQLQQPAQGQQGQQLAQGQQGQQPAQVQQGQQPAQGQQGQQLGQGQQQQQQQQPA 615
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01-MAR-1989 (Rel. 10, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Salivary acidic proline-rich phosphoprotein 1/2 precursor (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (Protein A/protein C) [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 PATQRQDPAAAQEGED-EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQE----MDPP 99
                                                                                                                                                                                                                                                                                                                                                                                 4 RGRSTYRP------RPRRYVEPPE-----MIGPMRPEQFS---DEVEPATPEEGE 44
                                                         GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                    24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ALLELES PRH2-1 AND PRH1-PIF).
MEDLINE-85289325; PubMed-2993301;
Maeda N., Kim H.-S., Azen E.A., Smithles O.;
"Differential RNA splicing and post-translational cleavages in the human salivary proline-rich protein gene system.";
J. Biol. Chem. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89061650; PubMed-3196309; MEDLINE-89061650; PubMed-3196309; MEDLINE-89061650; PubMed-3196309; Hay D.I., Bennick A., Schlesinger D.H., Minaguchi K., Madapallimattam G., Schluckebler S.K.; S.K.; Lipe primary structures of six human salivary acidic proline-rich proteins (PRP-1, PRP-2, PRP-3, PRP-4, PIF-s and PIF-f)."; Biochem. J. 255:15-21(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=88074309; PubMed=3687941;
Azen E.A., Kim H.S., Goodman P., Flynn S., Maeda N.;
"Alleles at the PRH1 locus coding for the human salivary-acidic proline-rich proteins Pa, Db, and PIF.";
Am. J. Hum. Genet. 41:1035-1047(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A. (ALLELES PRH1-4 AND PRH2-1).
SEQUENCE-86196106; PubMed-3009472;
Kim H.-S., Maeda N.;
"Structures of two HaelII-type genes in the human salivary proline-rich protein multigene family.";
J. Biol. Chem. 261:6712-6718(1986).
                                                                                                                                                                                                                                                       15.2%; Score 98; DB 1; Length 838; 22.8%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                    59; Indels
                                                                                                                                                            71D715B7BDF0722D CRC64;
Seed storage protein; Repeat; Multigene family;
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MEDLINE-86222916; PubMed-3710693;
                                                                                                                                                               838 AA; 89174 MW;
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Best Local Similarity
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EMBL; M13057; AAA98807.1; EMBL; M13058; AAA98808.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A frequent mutation in the acidic proline-rich protein gene, PRH2, causing a Q147X change closely adjacent to the bacterial binding domain of the cognate salivary PRP (Prl') in Afro-Americans."; Hum. Mutat. 12:72-72(1998).

-i- FUNCTION: PRP'S ACT AS HIGHLY POTENT INHIBITORS OF CRYSTAL GROWTH OF CALCIUM PHOSPHATES. THEY PROVIDE A PROTECTIVE AND REPARATIVE ENVIRONMENT FOR DENTAL ENAMEL WHICH IS IMPORTANT FOR THE INTEGRITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 17-122 (PROTEIN A).
Schlesinger D.H., Hay D.L.;
"Complete primary structure of a proline-rich phosphoprotein (PRP-4),
a potent inhibitor of calcium phosphate precipitation in human parotid
                                                                                                                                                                                                                                                                                                                                                                  woukey sallyary anionic proline-rich proteins.";
Int. J. Pept. Protein Res. 17:34-41(1981).
[8]
SEQUENCE OF 17-122 (PROTEIN A).
MEDLINE-79173237; PubMed=438215;
Wong R. S.C., Hofmann T., Bennick A.;
"The complete primary structure of a proline-rich phosphoprotein from human saliva.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECURNCE OF 123-166 (PEPTIDE P-C).
MEDLINE-80227634; PubMed=7390979;
ISEMURA S., Saltch E., Sanada K.;
"The amino acid sequence of a salivary proline-rich peptide, P-C, and its relation to a salivary proline-rich phosphoprotein, protein C.";
J. Biochem. 87:1071-1077(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYMORPHISM: ALLELE PRH1-4 IS ALSO KNOWN AS PRH1 DA ALLELE;
ALLELE PRH2-1 IS ALSO KNOWN AS PR1 OR PROTEIN C; ALLELE PRH2-3 IS
ALSO KNOWN AS PR1'.
Schlesinger D.H., Hay D.I.; "Complete covalent structure of a proline-rich phosphoprotein, PRP-2, an inhibitor of calcium phosphate crystal growth from human parotid
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THE TEETH.
THE PREVENT OF THE TEEVEN FROM PRP-2 BY POST-TRANSLATIONAL CLEAVAGE;
PRP-3 (PROTEIN A) IS DERIVED FROM PRP-1 BY POST-TRANSLATIONAL
CLEAVAGE. PIF-F IS DERIVED FROM PIF-S BY POST-TRANSLATIONAL
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Peptides: structure and biological function (Proceedings of the 6th
American peptide symposium), pp.133-136, Pierce Chemical Co.,
Rockford II. (1979).
                                            Int. J. Pept. Protein Res. 27:373-379(1986).
[6]
SEQUENCE OF 17-166 (PROTEIN C).
MEDLINE=80204368; PubMed=7380845;
Wong R.S.C. Bennick A.:
Withe primary structure of a salivary calcium-binding proline-rich phosphoprotein (protein C), a possible precursor of a related salivary protein A.";
J. Blol. Chem. 255:5943-5948(1980).
                                                                                                                                                                                                                                                                                                                                        Schlesinger D.H., Hay D.I.; "Primary structure of the active tryptic fragments of human and monkey salivary anionic proline-rich proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 254:4800-4808(1979).
                                                                                                                                                                                                                                                                                               SEQUENCE OF 17-46 (PROTEIN C).
MEDLINE=81191179; Pubmed=7228490;
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EMBL; K03202; AAA60183.1; -. EMBL; K03202; AAA60184.1; -.

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Gaps
                                                                      Signal; Parotid gland; Phosphorylation; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                              39 EQFIDEERQGPPLGG----QOSQPSAGDGNQDDGPQQGPPQQGGQQQQGPPPPQGKPQGP 94
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                                                                                                                                PEPTIDE P-C.
INHIBIT HYDROXYAPATITE FORMATION, BIND
                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                  ch 15.1%; Score 97.5; DB 1; Length 166; 1 Similarity 29.3%; Pred. No. 1; 29; Conservative 7; Mismatches 38; Indels 2;
                                                                                        SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2.
SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 3/4.
                                                                                                                                                                       PHOSPHORYLATION.
D -> N (IN ALLELE PRH1-4).
/FTIG=VAR_005563.
/FTIG=VAR_005563.
/FTIG=VAR_005564.
Q -> K (IN ALLELE PRH2-1).
/FTIG=VAR_005565.
F -> P (IN REF. 10).
W; A7DF62BF94E3G3FF CRC64;
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                PIR, A03290, PIHUSC.
PIR, JP0106, JP0106.
MIM, 168730, ...
MIM, 168710, ...
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 1, 2002, 06:32:13 ; Search time 21.85 Seconds (without alignments) 918.417 Million cell updates/sec

US-09-782-745-27 646 1 MSWRGRSIYRPRRRRYVEPP......DPPNPEEVKIPEEGEKQSQC 116 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_19:\* Database

sp\_rodent:\*
sp\_virus:\*
sp\_virus:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_ractoriap:\*
sp\_archeap:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	Ogueus homo sapien	Q9bss7 homo sapien	Q96qt9 homo sapien	036421 alcelaphine	018563 strongyloid	Q91164 arabidopsis	018564 strongyloid	Q91x93 mus musculu	Q9jm99 mus musculu	Q62882 rattus norv	Q62881 rattus norv	Q96gul homo sapien	Q62105 mus musculu	073450 human papil	Q64306 mus musculu	Q9jle8 mus musculu
SUMMARIES		ID	Q90E05	Q9BSS7	Q96GT9	036421	018563	Q9LJ64	018564	Q91x93	09JM99	062882	062881	Q96GU1	062105	073450	064306	Q9JLE8
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RESULT

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## ALIGNMENTS

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                                                                   Length 146;
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Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                     30; Indels
                                                                                                                                                 Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004861; AAH04861.1; -
SEQUENCE 146 AA; 16150 MW; E6C7BA94DB98DCB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009232; AAH09232.1; ..
SEQUENCE 111 AA; 12354 MW; 38C93332C5BA0E14 CRC64;
                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC:2001 (TrEMBLrel. 19, Last annotation update)
G ANTIGEN, FAMILY B, 1 (PROSTATE ASSOCIATED).
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Last annotation update)
                                                                                                                                                                                                                 Score 266; DB 4;
Pred. No. 1.1e-16;
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Best Local Similarity 45.8%
Matches 54; Conservative
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Eukaryota; Metazoa;
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Best Local Similarity
Matches 66; Conserv
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                                                                                                                                        TISSUE-MELANOMA.;
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                                                                                                        NCBI_TaxID=9606;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DRC-2001 (TrEMBLEL. 19, Last annotation update)
1GG AND IGE IMMUNOREACTIVE ANTIGEN RECOGNIZED BY SERA FROM PATIENTS
WITH STRONGYLOIDIASIS (FRAGMENT).
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"Primary structure of the alcelaphine herpesvirus 1 genome.";
J. Virol. 71:6517-6525(1997).
EMBL; AF005370; AAC56118.1; -
INTERPROS INTROBOO087; Collagen.
SEQUENCE 1300 AA; 128183 MW; 40F9EFD244F34577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1300;
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Panagrolaimoidea, Strongyloididae, Strongyloides.
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                                                                                     Alcelaphine herpesvirus 1 (wildebeest herpesvirus). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Ramachandran S., Thompson R.W., Gam A.A., Neva F.A.;
"A set of recombinant clones for immunodiagnosis of
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE IMMEDIATE EARLY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.4%; Score 119; DB 12;
35.2%; Pred. No. 0.015;
iive 7; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEGASAGQGPKPEAHSQEQGHPQTGCECEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                MEDLINE=97404659; PubMed=9261371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongyloides stercoralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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nes 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 PEEGEKQS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-EGECQS 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strongyloidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6248;
                                                                                                                                                                                                                                                                          STRAIN=C500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
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RESULT 036421

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**091J64** 

RESULT 09LJ64

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01-0CT-2000 (TEMBLrel. 15, Las
01-DEC-2001. (TEMBLrel. 19, Las
HYPOTHETICAL 116.0 KDA PROTEIN.
strongyloidiasis.";
Submitted (FBB-1997) to the EMI
EMBL: U90344; AAB65142.1; -.
InterPro; IPRO00087; Collagen.
                                                                                  144 AA; 15331 MW;
                                                                                                                                17.9%;
34.5%;
                                                                                                                                Query Match 17.99
Best Local Similarity 34.59
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEKQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 GPQQ 201
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01-0CT-2000
                                                                 NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               Q91X93
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Q9JM99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana chromosome 3. II.
4,251,695 bp covered by ninety Pl,
                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 PRPRRYVEPPEMIGPM-----RPEQFSDEV-----EPATPEEGEPATQRQDPAAAQE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
IGG AND IGE IMMUNOREACTIVE ANTIGEN RECOGNIZED BY SERA FROM PATIENTS
WITH STRONGYLODIASIS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                           Sato S., Nakamura Y., Asamizu E., Tabata S.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GEDEGASAGQ-GPKPEAHSQEQGHPQTGCECEDGP--DGQEMDPPNPEEVKTPE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 956;
64 A---GPEEPEGPEEPEG--PAGPEEPEGPEEPE-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAVODOXIN; UNKNOWN_1.
102822 MW; E34E185E63BB47C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukarýota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Ramachandran S., Thompson R.W., Gam A.A., Neva F.A.; "A set of recombinant clones for immunodiagnosis of
                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EXTENSIN PROPERIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.0%; Score 116.5; DB 27.2%; Pred. No. 0.018; tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 AA
                                                                                                 956 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura Y.;
"Structural analysis of Arabidopsis thal
"Structural analysis of Arabidopsis thal
Sequence features of the regions of 4,25
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP000735; BAB01698.1; -.
Interpro: IPR001265; Flavodoxin.
Interpro: IPR003592; LRR_Out.
InterPro: IPR003582; Pistil_extensin.
InterPro: IPR002965; P. rich_extensin.
InterPro: IPR002965; P. rich_extensin.
PRINTS; PR01217; PRICHEXTENSIN.
SMART; SM00370; LRR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00201; FLAVODOXIN;
SEQUENCE 956 AA; 102822 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           018564;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongyloides stercoralis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           Kaneko T., Kato T., S
Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-COLUMBIA;
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Best Local S
Matches 31)
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AC OC OC OC OX RA RA RA RT RT RA RT

RESULT 018564

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Gaps
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                                                                                                                                                                                                                                                                                      RSTYRPRPRRYVE-PPEMIGPMRPEQFSDEVEPATPEEGE-PATQRQDPAAAQEGEDEGA 63
                                                                                                                                                                                                                                                                                                                                     20 RPIVKPKPKTTTQAPEEPEGPEEPEGPEGPEGPEGPEGPAGPEEPEGPAGPEEPEGP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRSTYRPRPRRYVEPPEMIGPM - - - RPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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6
                                                                                                                                                                                   Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.3%; Score 112; DB 11; Length 504; 29.0%; Pred. No. 0.023; ative 13; Mismatches 57; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                           64 SAGQGP-KPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-SALIVARY GLAND;
TISSUE-SALIVARY GLAND;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; BC011176; AAH11176.1; -.
SEQUENCE 504 AA; 51775 MW; E4B9A3317FBEABF2 CRC64;
to the EMBL/GenBank/DDBJ databases
                                                                                                      894E20F248405592 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO PROLINE-RICH PROTEIN BSTNI SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                             1; Score 115.5; DB 5;
5; Pred. No. 0.0031;
14; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1054 AA
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                          7 STYRPRPRRYVEP-----PEMIGPMRPEQFS-DEVEPATPEEGEPATQRQDPAAAQEG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDEGASAGQGP----KPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVK--TPEEGE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RYVEPPEMIGPMRPEQFSDEVEPATPEEGE----PATQRQDPAAAQEGEDEGASAGQGPKP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PEP 95
                               Y.;
the mouse and human PRG4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geertman R., McMahon A. Sabban E.L.;

"Cloning and characterization of cDNAs for novel proteins with glutamic acid-proline dipeptide tandem repeats.";

Blochim. Biophys. Acta, Gene Struct. Expr. 1306:147-152(1996).

EMBL; 040628; AAB05668.1; -.

Hypothetical protein.

SEQUENCE 139 AA; 15459 MW; 60573DF693989709 CRC64;
                                                                                                                                                                                                                                                                                                                               Length 1054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.0%; Score 110; DB 11; Length 1 31.8%; Pred. No. 0.0092; Live 15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RASEEEIGGP - - - EDSEAVOPRTPEEPELEAEATKGDEPDLEQEMEPE - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00201; SO; 2.

SPOSITE; PS00024; HEMOPEXIN; UNKNOWN_1.

PROSTITE; PS00524; HEMOPEXIN_B; 2.

SEQUENCE 1054 AA; 115992 MW; 4FC64BFA42283235 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTP--EEGEKQSQC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                             17.2%; Score 111; DB 11;
30.3%; Pred. No. 0.061;
tive 17; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-SKELETAL MUSCLE; MEDLINE-96221285; PubMed-8634331;
           MEDLINE=20573856; PubMed=11124536; Ikegawa S., Sano M., Koshizuka Y., Nakamura "Isolation, characterization and mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                          (proteoglycan 4) genes.";
Cytogenet. Cell Genet. 90:291-297(2000)
EMBL; AB034730; BAA92310.1;
                                                                                                                    InterPro: IPR000585; Hemopexin.
InterPro: IPR002965; P_rich_extensn.
InterPro: IPR001212; Somatomedin_B.
Ffan; PF01033; Somatomedin_B. 2.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00120; HX.
SMART; SM00120; HX.
SMART; SM00201; SO, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 31.8%
nes 34; Conservative
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                        MGD; MGI:1891344; Prg4.
                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 36; Conserv
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Matches
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Q62882
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGA 63
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRAIN-SPRAGUE-DAWLEY, TISSUE-PHEOCHROMACYTOMA, AND BRAIN;

MEDLINE-96521285; PubMed-8634331;

Geertman R., McMahon A., Sabban E.L.;

Geortman R., McMahon A., Sabban E.L.;

"Cloning and characterization of cDNAs for novel proteins with glutamic acid-proline dipeptide tradem repeats";

Biochim. Biophys. Acta, Gene Struct. Expr. 1306:147-152(1996).

R EMBL: 1040627; AAB05667.1;

InterPro; IPRO1315; CARD.

SMART; SM00114; CARD; 1.

R PROSITE; PSS0209; CARD; 1.

Hypothetical protein.

SEQUENCE 221 AA; 24576 MW; A7661C9040B2CD4D CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.0%; Score 110; DB 11; Length 221; 31.8%; Pred. No. 0.015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009230; AAH09230.1; -
SEQUENCE 110 AA; 11777 MW; 6D6AF4563135BB6C CRC64;
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                                                                                                01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 24.6 KDA PROTEIN.
RATKUS NOTVEGICUS (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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221 AA.
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   PRT;
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PRELIMINARY;
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                              Q62881;
01-NOV-1996 (
01-NOV-1996 (
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Delius H., Saegling B., Bergmann K., Shamanin V., de Villiers E.M.;
"The genomes of three of four novel HPV types, defined by differences of their Li genes, show high conservation of the E7 gene and the
                                                                                                                                                                                                                                                                                                                                                                                                                   121 QGSSQQRPPQPGNQQGPPPQGGPQQRPPQPGNQQGP--PPPGGPQQRPPQPGGNQGPPQ 178
                                                                                                                                                                                                                                                                                                                                                                                                     GASAG-----QGPKPEAHSQ-----EQGHPQTGCECEDGPDG-----QEMDPPN 100
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                                                                                                                                                                                                                                                                                                                                                    4 RGRSTYR-PRPRRYVEPPEMIGP-MRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDE 61
                                                                                                                                                                                    Clements S., Mehansho H., Carlson D.M.; "Novel multigene families encoding highly repetitive peptide sequences: Sequence analyses of rat and mouse proline-rich protein
                   062105
062105
062105;
01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.DEC-2001 (TrEMBLrel. 19, Last sequence update)
31-KDA PROLINE-RICH SALIVARY PROTEIN OF CLONE PUMP125.
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                               30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.3%; Score 105.5; DB 12; Length 224; 27.0%; Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                   16.4%; Score 106; DB 11; Length 301; larity 29.3%; Pred. No. 0.047; Conservative 10; Mismatches 54; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type 76.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                    J. Biol. Chem. 260:13471-13477(1985).
EMBL; M11897; AAA40001.1; -.
SEQUENCE 301 AA; 31253 MW; 7F7D99A3F64C6E91 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 AA
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                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-86033799; PubMed-3840480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 240:359-365(1998).
EMBL; Y15174; CAA75462.1; -.
NOW_TER 1 1
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Matches 39; Conserv
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MEDLINE-92174915; PubMed-1339347;
MEDLINE-92174915; PubMed-1339347;
Layfield R., Bannister A., Plerce E.J., McDonald C.J.;
"CDNA clones for mouse parotid proline-rich proteins. mRNA regulation by isoprenaline and the nucleotide sequence of proline-rich protein
                                                             E------GASAGGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKT 106
                                                                                       17 RPRSYGDPPTPAPFPPTTPGPRRPPAQEPPQPTAPPALAPREHONSHPKPTPGKEGTE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 PRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPK 70
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 GGPQPGNQQGPPPQGGPQGPPRPGNQQGPPPQGGPQRPPQPGNHQ 241
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Last annotation update)
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                                                                                                                                                                                                                                                                                            260 AA
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                                                                                                                                                                                                                                                                                            PRT;
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EMBL; X63004; CAA44733.1; -.
MGD; MGI:1927478; Prpmp5.
SEOUENCE 260 AA; 26644 MW;
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17,
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
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Matches 31; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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(without alignments)
540.460 Million cell updates/sec
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2. /SIDS1/gcgdata/geneseqy-embl/AA1981.DAT:*
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8. /SIDS1/gcgdata/geneseqy-embl/AA1988.DAT:*
9. /SIDS1/gcgdata/geneseqy-embl/AA1988.DAT:*
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11. /SIDS1/gcgdata/geneseqy/geneseqp-embl/AA1989.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: /SIDS1/gcgdata
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. (SIDSI)/goddatu/genesedy/genesedy-embl./AA1991.DAT:
(SIDSI)/goddatu/genesedy/geneseqp-embl./AA1991.DAT:
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Description	GAGE2 polypeptide. GAGE4 polypeptide. GAGE5 polypeptide. GAGE5 polypeptide. GAGE6 tumour reje GAGE6 polypeptide. GAGE1 polypeptide. GAGE1 polypeptide. GAGE1 polypeptide. GAGE1 polypeptide. GAGE1 polypeptide.	GAGE3 polypeptide.
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SUMMARIES	AAY83159 AAW47599 AAY83162 AAY83163 AAY83164 AAY83164 AAY83160 AAW47603 AAW47603	AAY83161
	21 22 22 22 23 13 19	21
% Query Match Length DB	116 1116 1117 1117 1117 1118 1117 1118	118
% Query Match ]	100.0 908.8 906.5 905.3 904.9 904.8	92.3
Score	646 623.5 619.5 616.5 615.5 612.5 612.5 608.5	596.5
Result No.	100	11

GAGE-3 tumour reje Human secreted pro Human polypeptide Novel human diagno A human cancer-ass Human polypeptide	Human protein SEQ Human cell cycle a Human cell cycle a Human cell cycle a Human howel human diagno PAGE-4 polypeptide Human secreted pro PAGE1 polypeptide. Human secreted pro PAGE1 polypeptide. Juman NOV2 protein PAGE3 polypeptide. Green BHV-1 str Human pi60 polypeptide. Streptococcus equi Human pi60 polypeptide. Streptococcus pneu Toxoplasma gondii Streptococcus pneu Streptococcus pneu Streptococcus pneu Streptococcus pneu Drosophila melanog BOPI protein. Mus Drosophila melanog Human polypeptide. Toxoplasma gondii Novel human gland diagno Novel human diagno diag	
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## ALIGNMENTS

PAGE-4; MAGE; GAGE; reproduction; testis; prostate; fallopian tube; uterus; placenta; cancer; major histocompatibility complex; MHC; CTL; cytotoxic T lymphocyte; immunce response; antibody; drug delivery; immunoconjugate. AAY83159 standard; Protein; 116 AA. 24-JUL-2000 (first entry) GAGE2 polypeptide. AAY83159; AAY83159 RESULT 

(USSH ) US DEPT HEALTH & HUMAN SERVICES 99WO-US20046 98US-0098993 WO200012706-A1. 01-SEP-1998; 31-AUG-1999; 09-MAR-2000

Homo sapiens

ä Vasmatzis G, Lee Brinkmann U, Pastan I,

WPI; 2000-237869/20.

Isolated PAGE-4 protein and peptide used for inducing a cytotoxic T lymphocyte response and for raising antibodies which can be used to, detect the presence of PAGE-4 in cell samples or body tissues

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                                                                                                                                                                                                                                 reproductive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms.

An isolated PAGE-4 peptide Which induces a cytotoxic T imphocyte response when bound to a major histocompatibility complex (MHC) class I molecule or the isolated PAGE-4 protein can be used in immunogenic compositions to raise a cytotoxic T lymphocyte response prostate, uterus and testis. The nucleic acids encoding PAGE-4 or PAGE-4 peptide fragments can also be used in these compositions.

Antibodies against PAGE-4 and its peptide fragments can be used in detecting the presence of PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are not related to reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. The received in therapeutic applications, the received in the page of the presence of PAGE-4 can also be used to raise antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. The received in therapeutic applications, the received in the page of the received the received in the page of the presence of page and page of the received in the page of the page
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                                                                                                                                                                                                      is a gene preferentially expressed in normal male and female
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                                                           Disclosure; Figure la; 63pp; English.
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The present sequence represents a GAGB-2 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21).

The major difference between these proteins and GAGE-1 is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 cond is a maintain structure. The antigens can be used to diagnose malenomms, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into Dlood or urine can be observed and then used to confirm a diagnosis of melanomm using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants.
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                                                                                                           Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas
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Pred. No. 4.6e-52;
0; Mismatches 1;
  В;
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Van Den Eynde
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                                                                                                                                                                                                      Example 13; Fig 5; 60pp; English.
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99.1%;
Boon-Falleur T, Debacker O,
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Best Local Similarity 99.1
Matches 115; Conservative
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                                        1998-076905/07.
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                                                                N-PSDB; AAV18717
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                                                                                                                        reproductive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms.

In solated PAGE-4 peptide which induces a cytotoxic T in ymphocyte response when bound to a major histocompatibility complex (MHC) class I molecule or the isolated PAGE-4 protein can be used in immunogenic compositions to raise a cytotoxic T lymphocyte response prostate, uterus and testis. The nucleic acids encoding PAGE-4 or PAGE-4 peptide fragments can also be used in these compositions.

Antibodies against PAGE-4 and its peptide fragments can be used in checting the presence of PAGE-4 and PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are the nucleonal and the spread of cancerous reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of raise antibodies which are then used as the targeting group of raise antibodies which are then used as the targeting group of raise antibodies which are then used as the targeting group of raise antibodies which are then used as the targeting group of raise antibodies which are then used as the targeting group of raise
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                                                                                                                                                                                                                                                                                                                                                                                    immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems. The PAGE polypeptide shares sequence similarity with the GAGE and MAGE family
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                                                                                                  Disclosure; Figure la; 63pp; English.
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           WPI; 2000-237869/20
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AAY83163
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PAGE-4 is a gene preferentially expressed in normal male and female reproductive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms. An isolated PAGE-4 peptide which induces a cytotoxic T lymphocyte response when bound to a major histocompatibility complex (MHC) class I molecule or the isolated PAGE-4 protein can be used in immunosenic compositions to raise a cytotoxic T lymphocyte response against cells expressing PAGE-4 including cancer cells of the prostate, uterus and testis. The nucleic acids encoding PAGE-4 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGE-4 peptide fragments can also be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are not related to reproduction can be indicative of the spread of cancerous reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems. The PAGE family polypeptide shares sequence similarity with the GAGE and MAGE family
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                                                                                                                                                                                                                Isolated PAGE-4 protein and peptide used for inducing a cytotoxic {\tt T} lymphocyte response and for raising antibodies which can be used to detect the presence of PAGE-4 in cell samples or body tissues
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Pred. No. 2.4e-50;
2; Mismatches 1; Indels 1;
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(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                           Vasmatzis G,
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Figure la; 63pp; English.
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96.68;
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Matches 113; Conservative
                                                                Pastan I, Brinkmann U,
                                                                                                                                            WPI; 2000-237869/20
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The major difference between these proteins and GAGE-1 is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1. TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5 end is totally cifferent from the other GAGE cDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. The antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants.
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                                                                                                                                                                                                                                                                    Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful to
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Pred. No. 4.6e-50;
1; Mismatches 2; Indels 1;
                                                                                                                                                                               Boon-Falleur T, Debacker O, Van Den Eynde B;
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                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
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                                                                     97WO-US10850
                                                                                                       96US-0669161
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Best Local Similarity 96.6
Matches 113; Conservative
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PAGE-4 is a gene preferentially expressed in normal male and female reproductive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and placenta, ratio pattern makes it a target for uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms.

An isolated PAGE-4 peptide which induces a cytotoxic T proposyte response when bound to a major histocompatibility complex (MHC) class I molecule or the isolated PAGE-4 protein can be used in immunogenic compositions to raise a cytotoxic T lymphocyte response prostate, uterus and testis. The nucleic acids encoding PAGE-4 or PROSTATE, and the presence of PAGE-4 and inthese compositions.

Antibodies against PAGE-4 and its peptide fragments can be used in detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are not related to reproduction can be indicative of the spread of cancerous reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of immunocularity and intention and in the presence of page-4 can also be used to raise immunocularity and prompted in the presence of page-4 can also be used to raise immunocularity and the presence of page-4 can also be used to raise immunocularity.
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                                                                                                                                                                                                                                                                                                                                 Vasmatzis G, Lee
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Matches 112; Conservative
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09-MAR-2000.
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Homo sapiens.
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An isolated PAGE-4 peptide which induces a cytotoxic T pumphocyte response when bound to a major histocompatibility complex. WHC) class I molecule or the isolated PAGE-4 protein can be used in immunogenic compositions to raise a cytotoxic T lymphocyte response gapinst cells expressing PAGE-4 including cancer cells of the prostate, uterus and testis. The nucleic acids encoding PAGE-4 or PAGE-4 peptide fragments can also be used in these compositions. Antibodies against PAGE-4 and its peptide fragments can be used in detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are not related to reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems. The PAGE antily
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                                                                                                                                                                                                                                                                      Isolated PAGE-4 protein and peptide used for inducing a cytotoxic T lymphocyte response and for raising antibodies which can be used to detect the presence of PAGE-4 in cell samples or body tissues
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94.9%; Score 613; DB 21; Length 118;
Best Local Similarity 97.4%; Pred. No. 9.9e-50;
Matches 111; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                    Lee
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                                                                                                                                                                                                Vasmatzis G,
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           WO200012706-A1
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The present sequence represents a GAGE-5 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5 end is totally different from the other GAGE CDNAS for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic 7 cell clone. Confirm adiagnosis of melanoma using cytolytic 7 cell clone. Proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. skin graft or organ transplants.
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Pred. No. 1.1e-49;
2; Mismatches 2; Indels 1;
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                                                                     /note= "Ala encoded by GAG"
                                                                                                                                           /note- "Thr encoded by CCT"
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Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
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94.8%;
Best Local Similarity 95.7%;
Matches 112; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0669161.
                                                                                                                                                                                                                                                                                                                                                               97WO-US10850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-076905/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnose melanomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV18720
                                  Misc-difference
                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                           23-JUN-1997;
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Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas
                                      GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation;
            GAGE-1 tumour rejection antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Fig 5; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                 Boon-Falleur T, Debacker O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-076905/07.
                                                                                                                                                             Misc-difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV05540
                                                                               HLA-typing assay.
                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                  WO9749417-A1
                                                                                                                                                                                                                                                                                                                  23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                  24-JUN-1996;
                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                  31-DEC-1997.
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ID AAY8
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 mswrgrstyywprprryvqppevigpmrpeqfsdevepatpeegepatqrqdpaaaqege 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful to diagnose melanomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC 116
 GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degasagggpkpeadsqegghpqtgcecedgpdgqevdppnpeevktpeegekqsqc 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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-4 No. 2.6e-49; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                          Van Den Eynde B;
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3; Mismatches
                                                                                                                                                                      /note= "Thr encoded by CCT"
                                                                                                                                        'note= "Ala encoded by GAG"
                                                                                             Location/Qualifiers Misc-difference 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW47598 standard; Protein; 138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 13; Fig 5; 60pp; English.
                                                                                                                                                                                                                                                                                                                                         LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.2%;
                                                                                                                                                                                                                                                                                                                                                                          Debacker O;
                                                                                                                                                                                                                                                                                                           96US-0669161
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N-PSDB; AAV18721.
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Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                                                                                                         Misc-difference 40
                                      HLA-typing assay.
                                                                                                                                                                                                                                                                                                                                                                          Boon-Falleur T,
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                                                                                                                                                                                                                                                                           23-JUN-1997;
                                                                                                                                                                                                                                                                                                           24-JUN-1996;
                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW47598
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Van Den Eynde B;

/note= "encoded by CCT" 'note= "encoded by GAG' Location/Qualifiers

97WO-US10850. 96US-0669161.

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The present sequence represents a GAGE-1 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testis. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 of TRAP sequence. The rest of the sequences show mismatches at various position, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAS for the first 112 bases. This credion of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melanomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic T cell clone proliferation methodologies. Other uses for the processed peptides, include HLA-typing assays for, e.g. SKin graft or organ transplants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EGASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 egasagggpkpeadsgegghpqtgcecedgpdggemdppnpeevktpee 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 598; DB 19;
Pred. No. 2.9e-48;
0; Mismatches 1;
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Best Local Similarity 99.1%;
Matches 108; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AA;
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GAGE tumour tumour rejection antigen precursor; TRAP; tumour; diagnosis; melanoma; antigen; cytolytic T cell clone proliferation; HLA-typing assay.

GAGE-3 tumour rejection antigen precursor.

(first entry)

30-JUL-1998

AAW47600;

AAW47600 standard; Protein; 118 AA

AAW47600 ID AAW4 XX

/note- "Ala encoded by GAG" /note- "Thr encoded by CCT"

Location/Qualifiers

Key Misc-difference 40

Homo sapiens

Misc-difference

WO9749417-A1

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PAGE-4 is a gene preferentially expressed in normal male and female reproductive tissues e.g. prostate, testis, fallopian tube, uterus and placenta, as well as in prostate cancer, testicular cancer and placenta, as well as in prostate cancer, testicular cancer and uterine cancer. This expression pattern makes it a target for diagnosis and for vaccine based therapy of such neoplasms.

An isolated PAGE-4 peptide which induces a cytocoxic T jumphocyte response when bound to a major histocompatibility complex (MHC) class I molecule or the isolated PAGE-4 protein can be used in immonogenic compositions to raise a cytocoxic T jumphocyte response against cells expressing PAGE-4 including cancer cells of the prostate, uterus and testis. The nucleic acids encoding PAGE-4 or PAGE-4 peptide fragments can also be used in these compositions.

Antibodies against PAGE-4 and its peptide fragments can be used in detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell samples or body tissues. The presence of PAGE-4 in tissues which are concertual tespecial can be indicative of the spread of cancerous reproductive tissue. PAGE-4 can also be used to raise antibodies which are then used as the targeting group of immunoconjugates comprising toxins used in therapeutic applications. This has applications for drug delivery systems. The PAGE and MAGE family concerned to reproductive tissues used in therapeutic applications.
                                                                                                                                                                                                                                                              PAGE-4; MAGE; GAGE; reproduction; testis; prostate; fallopian tube; uterus; placenta; cancer; major histocompatibility complex; MHC; CTL; cytotoxic T lymphocyte; immunce response; antibody; drug delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated PAGE-4 protein and peptide used for inducing a cytotoxic T lymphocyte response and for raising antibodies which can be used to detect the presence of PAGE-4 in cell samples or body tissues
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                                                                                        24-JUL-2000 (first entry)
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                                                                                                                                                                                SAGE3 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                 immunoconjugate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40200012706-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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AAY83161;
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Isolated nucleic acid encoding GAGE tumour rejection antigen precursor - processed by HLA-Cw6 molecules into peptides, useful diagnose melanomas

Example 13; Fig 5; 60pp; English.

Debacker O, Van Den Eynde

WPI; 1998-076905/07. N-PSDB; AAV18718.

Boon-Falleur T,

(LUDW-) LUDWIG INST CANCER RES

97WO-US10850 96US-0669161

23-JUN-1997; 24 - JUN - 1996;

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The present sequence represents a GAGE-3 tumour tumour rejection antigen precursor (TRAP). The protein is expressed in a number of tumours. In contrast the only normal tissue which expresses GAGE TRAP protein is testia. Several GAGE TRAPs have been identified (see AAV18717-21). The major difference between these proteins and GAGE-1 is the absence of a stretch of 143 bases located at position 379 to 521 of the GAGE-1 TRAP sequence. The rest of the sequences show mismatches at various osition, with the exception of GAGE-3 whose 5' end is totally different from the other GAGE CDNAs for the first 112 bases. This region of GAGE-3 cDNA contains a long repeat and a hairpin structure. The antigens can be used to diagnose melalomas, characterised by expression of a TRAP or presentation of a tumour rejection antigen. Antigens shed into blood or urine can be observed and then used to confirm a diagnosis of melanoma using cytolytic cell clone. Confirm a diagnosis of melanoma using cytolytic real clone. Proteistation methodologies. Other uses for the processed peptides, include HIA-typing assays for, e.g. skin graft or organ transplants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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Pred. No. 1.5e-47;
3; Mismatches 2;
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Best Local Similarity 94.7%;
Matches 108; Conservative
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Gaps

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RGRST-YRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEG 62

Query Match 92.3%; Score 596.5; DB 21; Length 118; Best Local Similarity 95.6%; Pred. No. 3.4e-46; Matches 109; Conservative 3; Mismatches 1, Indels 1;

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63 ASAGQGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQC 116

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Albahimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                            Human polypeptide SEQ ID NO 2733.
                                                                                                                                                                                                                                                                                                  26-DEC-2000; 2000WO-US34263.
               22-OCT-2001 (first entry)
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N-PSDB; AAI58744.
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09-JUL-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
14-SEP-2000; 2
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29-NOV-2000;
                                                                                                                                                                                                      Homo sapiens.
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Zhao QA,
                                                                                                                                                                    Leukaemia.
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Matches
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Dp
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0
                                                                                                                                                                                                      sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs derived from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 MIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEDEGASAGQGPKPEAHSQEQGHP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 400; DB 21; Length 76;
Pred. No. 4e-30;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID 6204; 71pp + CD-ROM; English.
                                                                                                                                                                        Human secreted protein, SEQ ID NO: 6204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM39588 standard; Protein; 111 AA.
                                                                      AAG02123 standard; Protein; 76 AA.
                                                                                                                                                                                                                          gene therapy; chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.9%;
illarity 97.3%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                             99US-0122487
                                                                                                                                        (first entry)
                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 QTGCECEDGPDGQEM 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC02129
                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                        5' EST;
                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999;
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                             EP1033401-A2
                                                                                                                                        06-OCT-2000
                                                                                                                                                                                                                                                                                                                             06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM39588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                      AAG02123;
                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM39588
                                                      AAG02123
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Wang D;

Ren F, W Zhang J;

Qian XB, Yang Y,

Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;

Liu C, Wang Z,

2000US-0488725. 2000US-0552117. 2000US-058042. 2000US-0620312. 2000US-065450. 2000US-0662191.

2000US-0727344

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                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPA--TPEEGEPATQRQDPAAAQE- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.0%; Score 271.5; DB 22; Length 111; 50.0%; Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
Example 4; SEQ ID NO 2733; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Best Local S
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymerased are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving applement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) and (II) are useful for treating classories involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed setting, with was obtained in electronic format directly from WIPO application, which was obtained in electronic format directly from WIPO application.
53 eedggaaetqvpdleadlgelsgsktggecgngpddggkilpksegfkmpeggdrgpg 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 35656; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #5288.
                                                                                                                                                                                                               ABG05297 standard; Protein; 112 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                    ABG05297;
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                                                                                                                                                                      ABG05297
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41.6%; Score 268.5; DB 22; Length 112; 49.2%; Pred. No. 1e-17; ive 14; Mismatches 35; Indels 11; Gaps

Query Match
Best Local Similarity 49.2%
Matches 58; Conservative

δ g

1 MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPA--TPEEGEPATQRQDPAAAQE- 57

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58 GEDEGASAGGGPKPEAHSQEQGHPQTGCECEDGPDGQEMDPPNPEEVKTPEEGEKQSQ 115
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Search completed: July 1, 2002, 06:32:09 Job time: 301 sec

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